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OM protein - protein search, using sw model

Run on: May 27, 2004, 15:46:47 ; Search time 39 Seconds

(without alignments)  
2470.284 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858  
Sequence: 1 MSFLGLLVTSALAGRGRT.....DVLEHHECDVCGRSGTG 345

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*
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- 6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep:\*
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- 17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	9	US-09-818-943-1
2	1858	100.0	345	9	US-09-852-209A-3
3	1858	100.0	345	12	US-10-439-337A-3
4	1858	100.0	345	12	US-10-303-997B-3
5	1858	100.0	345	13	US-10-086-623-32
6	1858	100.0	345	14	US-10-260-539-32
7	1858	100.0	345	14	US-10-131-600-3
8	1851	99.6	345	9	US-09-823-033-2
9	1851	99.6	345	9	US-09-923-995-4
10	1851	99.6	345	9	US-09-795-006A-149
11	1851	99.6	345	9	US-09-978-285A-488
12	1851	99.6	345	9	US-09-978-697-488
13	1851	99.6	345	9	US-09-978-192A-488
14	1851	99.6	345	9	US-09-999-832A-488
15	1851	99.6	345	10	US-09-978-189-488

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42	1851	99.6	345	11	US-09-876-813-33
43	1851	99.6	345	12	US-10-147-493-286
44	1851	99.6	345	12	US-10-164-749A-488
45	1851	99.6	345	12	US-10-145-127-286

#### ALIGNMENTS

RESULT 1  
US-09-818-943-1  
Sequence 1, Application US/09818943  
Patent No. US20020049987A1  
GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: LI, Xuri  
APPLICANT: PONTEN, Annica  
APPLICANT: MASE, Karin  
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH  
FILE REFERENCE: 1064/48487  
CURRENT APPLICATION NUMBER: US/09/818, 943  
CURRENT FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: US 60/192,507  
PRIOR FILING DATE: 2000-03-28  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-818-943-1

Query Match 100.0%; Score 1858; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6.8e-179; Indels 0; Gaps 0;  
Matches 345; Conservative 0; Mismatches 0;

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1 MSFLGLLVTSALAGRGRTQAESNLSKFPSSKNGQVDPQHRITVSTNGSIHS 60  
1 PRPHTYPRNTVTLVWRLVAEENWVLTDFDERFGLDPEDDICKYFVEEYPSDGTIL 120  
1 PRPHTYPRNTVTLVWRLVAEENWVLTDFDERFGLDPEDDICKYFVEEYPSDGTIL 120  
61 PRPHTYPRNTVTLVWRLVAEENWVLTDFDERFGLDPEDDICKYFVEEYPSDGTIL 120  
121 GRWGSSTVPGKSKNQIRIRFVSDYFPESEGFCHINIVMPQTEAVSPVLPPSA 180

Db 121 GRWGSCTVPGKQISKNQIRIRFVSDYEPSEBPGFICHINIVMPQFTEAVSPSVLPSPA 180  
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Db 181 LPDLNNATITASTLEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDLNL 240  
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Db 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300  
QY 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345  
Db 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345

## RESULT 2

US-09-852-209A-3  
Sequence 3, Application US/09852209A  
Patent No. US20020164687A1  
GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: AASE, Karin  
APPLICANT: LEE, Xuri  
APPLICANT: PONTEN, Annica  
APPLICANT: TUTELA, Marko  
APPLICANT: ALITALO, Kari  
APPLICANT: OESTMAN, Arne  
APPLICANT: HELDIN, Carl-Henrik  
APPLICANT: BETHSHOLTZ, Christel  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
CURRENT APPLICATION NUMBER: US/09/852,209A  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/410,349  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 60/110,749  
PRIOR FILING DATE: 1998-12-03  
PRIOR APPLICATION NUMBER: 60/113,002  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: 60/135,426  
PRIOR FILING DATE: 1999-05-21  
PRIOR APPLICATION NUMBER: 60/144,022  
PRIOR FILING DATE: 1999-07-15  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-852-209A-3

Query Match 100.0%; Score 1858; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6,8e-179;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MSIFGLLVTSALAGRGTOAESNLSSKQFSSNKEQGVDPQHERITTVSTNGSIHS 60  
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Db 61 PREPHYPRNTVLMVRLVAEENVMQLTFDERFGLEDDEDDICKYDFVEVEPSDGTIL 120  
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Db 121 GRWGSCTVPGKQISKNQIRIRFVSDYEPSEBPGFICHINIVMPQFTEAVSPSVLPSPA 180  
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Db 181 LPDLNNATITASTLEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDLNL 240

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Db 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300  
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Db 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345

## RESULT 3

US-10-439-337A-3  
Sequence 3, Application US/10439337A  
Publication No. US20040053837A1  
GENERAL INFORMATION:  
APPLICANT: Li, Xuri  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: CARMELIET, Peter  
TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND  
FILE REFERENCE: 029065,44740C4  
CURRENT APPLICATION NUMBER: US/10/439,337A  
CURRENT FILING DATE: 2003-05-16  
PRIOR APPLICATION NUMBER: US 10/303,997  
PRIOR FILING DATE: 2002-11-26  
PRIOR APPLICATION NUMBER: US 09/410,349  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: US 60/102,461  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: US 60/108,109  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/110,749  
PRIOR FILING DATE: 1998-12-03  
PRIOR APPLICATION NUMBER: US 60/113,002  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: US 60/135,426  
PRIOR FILING DATE: 1999-05-21  
PRIOR APPLICATION NUMBER: US 60/144,022  
PRIOR FILING DATE: 1999-07-15  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-439-337A-3

Query Match 100.0%; Score 1858; DB 12; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6,8e-179;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MSIFGLLVTSALAGRGTOAESNLSSKQFSSNKEQGVDPQHERITTVSTNGSIHS 60  
QY 61 PREPHYPRNTVLMVRLVAEENVMQLTFDERFGLEDDEDDICKYDFVEVEPSDGTIL 120  
Db 61 PREPHYPRNTVLMVRLVAEENVMQLTFDERFGLEDDEDDICKYDFVEVEPSDGTIL 120  
QY 121 GRWGSCTVPGKQISKNQIRIRFVSDYEPSEBPGFICHINIVMPQFTEAVSPSVLPSPA 180  
Db 121 GRWGSCTVPGKQISKNQIRIRFVSDYEPSEBPGFICHINIVMPQFTEAVSPSVLPSPA 180  
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Db 181 LPDLNNATITASTLEDLIRYLEPERWQDLEDLYRPTWQGLGKAFVGRKSRVVDLNL 240  
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Db 241 LTBEBRLVYCTPRNFSVSIREEBKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSPK 300  
QY 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345  
Db 301 VTKKHEVILQLRPKTGVGRGLHKSITDVALHHEBECDCVCRGSTGG 345

Db 301 VTKKYHEVLQLRPKTVGRGLHKSILTDVALHEHHECDVCVCRSGTGG 345

## RESULT 4

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US-10-303-997B-3
; Sequence 3, Application US/10303997B
; Publication No. US20030211994A1
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELET, Peter
; APPLICANT: COLLUM, Desire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.4474003
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-303-997B-3

Query Match      100.0%; Score 1858; DB 12; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.8e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSFLGGLLVTSALAGRRGTOAESNLSSKFOFSSNKKEONGVODPOHERIITVSTNGSIHS 60
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Db 61 PRPHYTPRNTVLVWRLVAABENWVQLTFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120
Cy 121 GRWCGSGTVGKQISKNOIRIRFVSDYFSPBEGFCIHNIWMPQTEAVSPSVLPESA 180
Db 121 GRWCGSGTVGKQISKNOIRIRFVSDYFSPBEGFCIHNIWMPQTEAVSPSVLPESA 180
Cy 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELYRPTQQLGKAFVFGKSRVVDNL 240
Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELYRPTQQLGKAFVFGKSRVVDNL 240
Cy 241 LTBEEVRLYSTCPNRFVSISIRELKRDTITIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTBEEVRLYSTCPNRFVSISIRELKRDTITIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Cy 301 VTKKYHEVLQLRPKTVGRGLHKSILTDVALHEHHECDVCVCRSGTGG 345
Db 301 VTKKYHEVLQLRPKTVGRGLHKSILTDVALHEHHECDVCVCRSGTGG 345

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## RESULT 5

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US-10-086-623-32
; Sequence 32, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf

```

APPLICANT: AASE, Karin

APPLICANT: LI, Xuri

APPLICANT: PONTEN, Annica

APPLICANT: UTTELA, Maiko

APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Arne

APPLICANT: HELDIN, Carl-Henrik

TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES 1

FILE REFERENCE: 1064/44833C2

CURRENT APPLICATION NUMBER: US/10/086,623

CURRENT FILING DATE: 2000-03-04

PRIOR APPLICATION NUMBER: US 60/107,852

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 60/113,997

PRIOR FILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: US 60/150,604

PRIOR FILING DATE: 1999-08-26

PRIOR APPLICATION NUMBER: US 60/157,108

PRIOR FILING DATE: 1999-10-04

PRIOR APPLICATION NUMBER: US 60/157,756

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 09/438,046

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US 09/691,200

PRIOR FILING DATE: 2000-10-19

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.1

SEQ ID NO 32

LENGTH: 345

TYPE: PRF

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: misc feature

OTHER INFORMATION: Amino acid sequence for PDGF-C

US-10-086-623-32

Query Match 100.0%; Score 1858; DB 13; Length 345;

Best Local Similarity 100.0%; Pred. No. 6.8e-179;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MSFLGGLLVTSALAGRRGTOAESNLSSKFOFSSNKKEONGVODPOHERIITVSTNGSIHS 60

Db 1 MSFLGGLLVTSALAGRRGTOAESNLSSKFOFSSNKKEONGVODPOHERIITVSTNGSIHS 60

Cy 61 PRPHYTPRNTVLVWRLVAABENWVQLTFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120

Db 61 PRPHYTPRNTVLVWRLVAABENWVQLTFDERFGLDEPDDICKYDFVEVEBPSDGTIL 120

Cy 121 GRWCGSGTVGKQISKNOIRIRFVSDYFSPBEGFCIHNIWMPQTEAVSPSVLPESA 180

Db 121 GRWCGSGTVGKQISKNOIRIRFVSDYFSPBEGFCIHNIWMPQTEAVSPSVLPESA 180

Cy 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELYRPTQQLGKAFVFGKSRVVDNL 240

Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELYRPTQQLGKAFVFGKSRVVDNL 240

Cy 241 LTBEEVRLYSTCPNRFVSISIRELKRDTITIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300

Db 241 LTBEEVRLYSTCPNRFVSISIRELKRDTITIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300

Cy 301 VTKKYHEVLQLRPKTVGRGLHKSILTDVALHEHHECDVCVCRSGTGG 345

Db 301 VTKKYHEVLQLRPKTVGRGLHKSILTDVALHEHHECDVCVCRSGTGG 345

## RESULT 6

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US-10-260-539-32
; Sequence 32, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri

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APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
FILE REFERENCE: 1064/44833C2
CURRENT APPLICATION NUMBER: US/10/260,539
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US/10/086,623
PRIOR FILING DATE: 2000-03-04
PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 60/113,997
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: US 60/150,604
PRIOR FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: US 60/157,108
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: US 60/157,756
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 09/438,046
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 09/691,200
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentln version 3.1
SEQ ID NO 32
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-260-539-32
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Query Match 100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 6,8e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSLAAGRGTOAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNSIHS 60
DB 1 MSIFGLLVTSLAAGRGTOAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNSIHS 60
QY 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHNYIMVPOFTEAVSPSVLP 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHNYIMVPOFTEAVSPSVLP 180
QY 181 LPDLNNATITAFSTEDLIRYLEPERRWQDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNATITAFSTEDLIRYLEPERRWQDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240
QY 241 LEEVRLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCEQCVP 300
DB 241 LEEVRLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCEQCVP 300
QY 301 VTKKYHEVLQLRPKTGVRLGHSKSLTDVALEHHEBCDCVCRGSTGG 345
DB 301 VTKKYHEVLQLRPKTGVRLGHSKSLTDVALEHHEBCDCVCRGSTGG 345
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RESULT 7
US-10-131-600-3
Sequence 3, Application US/10131600
Publication No. US20030082670A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
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APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETHSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
FILE REFERENCE: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/10/131,600
PRIOR FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/108,109
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 3
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-600-3
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Query Match 100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 6,8e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSLAAGRGTOAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNSIHS 60
DB 1 MSIFGLLVTSLAAGRGTOAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNSIHS 60
QY 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
DB 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDDEDDICKYDFVEEPPSDGTL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHNYIMVPOFTEAVSPSVLP 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDYFSPGFCIHNYIMVPOFTEAVSPSVLP 180
QY 181 LPDLNNATITAFSTEDLIRYLEPERRWQDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNATITAFSTEDLIRYLEPERRWQDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240
QY 241 LEEVRLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCEQCVP 300
DB 241 LEEVRLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCEQCVP 300
QY 301 VTKKYHEVLQLRPKTGVRLGHSKSLTDVALEHHEBCDCVCRGSTGG 345
DB 301 VTKKYHEVLQLRPKTGVRLGHSKSLTDVALEHHEBCDCVCRGSTGG 345
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RESULT 8
US-09-823-033-2
Sequence 2, Application US/09823033
Patent No. US2002004225A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
FILE REFERENCE: 00-12
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
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SOFTWARE: FASTSEQ for Windows version 3.0  
 SEQ ID NO 2  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-823-033-2

Query Match 99.6%; Score 1851; DB 9; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 3.5e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60  
 DB 1 MSLEGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60  
 QY 61 PRPHYPRNTVWLVRLVAEENWVQLTDFERFGLDEPDICKYDVEVEEPESDGTL 120  
 DB 61 PRPHYPRNTVWLVRLVAEENWVQLTDFERFGLDEPDICKYDVEVEEPESDGTL 120  
 QY 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFSPSEPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 DB 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFSPSEPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 QY 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKSRVVDLNL 240  
 DB 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKSRVVDLNL 240  
 QY 241 LTBVRLVYSCTRPNFVSISIRELKRDTITFWPGCLLVRCGNCACCLHNCOCVPSK 300  
 DB 241 LTBVRLVYSCTRPNFVSISIRELKRDTITFWPGCLLVRCGNCACCLHNCOCVPSK 300  
 QY 301 VTKKYHEVLQLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345  
 DB 301 VTKKYHEVLQLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345

RESULT 9  
 US-09-923-995-4  
 Sequence 4, Application US/09923995  
 Patent No. US20020081700A1  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1  
 FILE REFERENCE: 00-47  
 CURRENT APPLICATION NUMBER: US/09/923,995  
 PRIOR FILING DATE: 2001-08-07  
 PRIOR APPLICATION NUMBER: US 60/223,164  
 PRIOR FILING DATE: 2000-08-07  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: FASTSEQ for Windows Version 3.0  
 SEQ ID NO 4  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-923-995-4

Query Match 99.6%; Score 1851; DB 9; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 3.5e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60  
 DB 1 MSLEGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60  
 QY 61 PRPHYPRNTVWLVRLVAEENWVQLTDFERFGLDEPDICKYDVEVEEPESDGTL 120  
 DB 61 PRPHYPRNTVWLVRLVAEENWVQLTDFERFGLDEPDICKYDVEVEEPESDGTL 120  
 QY 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFSPSEPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 DB 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFSPSEPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 QY 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKSRVVDLNL 240

DB 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKSRVVDLNL 240  
 QY 241 LTBVRLVYSCTRPNFVSISIRELKRDTITFWPGCLLVRCGNCACCLHNCOCVPSK 300  
 DB 241 LTBVRLVYSCTRPNFVSISIRELKRDTITFWPGCLLVRCGNCACCLHNCOCVPSK 300  
 QY 301 VTKKYHEVLQLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345  
 DB 301 VTKKYHEVLQLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345

RESULT 10  
 US-09-795-006A-149  
 Sequence 149, Application US/09795006A  
 Patent No. US20020151680A1  
 GENERAL INFORMATION:  
 APPLICANT: Allcalo et al  
 TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
 FILE REFERENCE: 28967/35977B  
 CURRENT APPLICATION NUMBER: US/09/795,006A  
 PRIOR FILING DATE: 2001-02-26  
 PRIOR APPLICATION NUMBER: US 60/205,331  
 PRIOR FILING DATE: 2000-05-18  
 PRIOR APPLICATION NUMBER: US 60/185,205  
 NUMBER OF SEQ ID NOS: 175  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 149  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-795-006A-149

Query Match 99.6%; Score 1851; DB 9; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 3.5e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60  
 DB 1 MSLEGLLIVTSALAGORRGTQAESNLSSKFOFSSNKEONGVDPQHERIITVSTNGSIHS 60  
 QY 61 PRPHYPRNTVWLVRLVAEENWVQLTDFERFGLDEPDICKYDVEVEEPESDGTL 120  
 DB 61 PRPHYPRNTVWLVRLVAEENWVQLTDFERFGLDEPDICKYDVEVEEPESDGTL 120  
 QY 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFSPSEPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 DB 121 GRMGSGTVPGKQISKGNOIRIRFVSDYFSPSEPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 QY 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKSRVVDLNL 240  
 DB 181 LPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKSRVVDLNL 240  
 QY 241 LTBVRLVYSCTRPNFVSISIRELKRDTITFWPGCLLVRCGNCACCLHNCOCVPSK 300  
 DB 241 LTBVRLVYSCTRPNFVSISIRELKRDTITFWPGCLLVRCGNCACCLHNCOCVPSK 300  
 QY 301 VTKKYHEVLQLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345  
 DB 301 VTKKYHEVLQLRPKTGVRLGHLKSLTDVALBHHBECDCVCRSGTGG 345

RESULT 11  
 US-09-978-295A-488  
 Sequence 488, Application US/09978295A  
 Patent No. US20020156006A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Deenoyere, Luc

APPLICANT: Baton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Pong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gettelsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
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PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-03-25  
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PRIOR APPLICATION NUMBER: 60/079920

PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-04-09  
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PRIOR FILING DATE: 1998-04-15  
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PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
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PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29

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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;  
Best Local Similarity 99.4%; Pred. No. 3, Se-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 MSLFGLLVTSALAGQRRGTQAESNLSSKFPQSSNKEQNGVDDPQHERITITVSTNGSIHS 60  
1 MSLFGLLVTSALAGQRRGTQAESNLSSKFPQSSNKEQNGVDDPQHERITITVSTNGSIHS 60  
61 PRPPTTYRNTVYLVRLVAEENWVIOQLTPDRFLEDEPBEDICRYDVEVEEESDGTIL 120  
61 PRPPTTYRNTVYLVRLVAEENWVIOQLTPDRFLEDEPBEDICRYDVEVEEESDGTIL 120  
121 GRWGCGTVPGKQISKGNOIRIRFVSDVEYFSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180  
121 GRWGCGTVPGKQISKGNOIRIRFVSDVEYFSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180  
121 GRWGCGTVPGKQISKGNOIRIRFVSDVEYFSEPGFCIHYNIVMPQFTEAVSPVLPPSA 180  
181 LPDLINNAITAFSTLEDLIRYLBERRWQDLEDLYRPTWQLGKAFVFGKRSRVVDNL 240  
181 LPDLINNAITAFSTLEDLIRYLBERRWQDLEDLYRPTWQLGKAFVFGKRSRVVDNL 240  
241 LEEVRLVSCTRPNRSVSIRELKRTPITFWPGCLVVRGCGNCCCLHNCNCCQVSK 300  
241 LEEVRLVSCTRPNRSVSIRELKRTPITFWPGCLVVRGCGNCCCLHNCNCCQVSK 300  
301 VTKKYHEVTLQRPKTGVGLHKSITDVALHHEBECDCVCRSGSTG 345

DB 301 VTKKYHEVTLQRPKTGVGLHKSITDVALHHEBECDCVCRSGSTG 345  
RESULT 12  
US-09-978-697-488  
Sequence 488, Application US/0978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25

PROR APPLICATION NUMBER: 60/079656  
PROR FILING DATE: 1998-03-26  
PROR APPLICATION NUMBER: 60/079664  
PROR FILING DATE: 1998-03-27  
PROR APPLICATION NUMBER: 60/079689  
PROR FILING DATE: 1998-03-27  
PROR APPLICATION NUMBER: 60/079663  
PROR FILING DATE: 1998-03-27  
PROR APPLICATION NUMBER: 60/079728  
PROR FILING DATE: 1998-03-27  
PROR APPLICATION NUMBER: 60/079786  
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PROR FILING DATE: 1998-03-31  
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PROR FILING DATE: 1998-03-31  
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PROR FILING DATE: 1998-04-01  
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PROR APPLICATION NUMBER: 60/081070  
PROR FILING DATE: 1998-04-08  
PROR APPLICATION NUMBER: 60/081049  
PROR FILING DATE: 1998-04-08  
PROR APPLICATION NUMBER: 60/081071  
PROR FILING DATE: 1998-04-08  
PROR APPLICATION NUMBER: 60/081195  
PROR FILING DATE: 1998-04-08  
PROR APPLICATION NUMBER: 60/081203  
PROR FILING DATE: 1998-04-09  
PROR APPLICATION NUMBER: 60/081229  
PROR FILING DATE: 1998-04-09  
PROR APPLICATION NUMBER: 60/081955  
PROR FILING DATE: 1998-04-15  
PROR APPLICATION NUMBER: 60/081817  
PROR FILING DATE: 1998-04-15  
PROR APPLICATION NUMBER: 60/081819  
PROR FILING DATE: 1998-04-15  
PROR APPLICATION NUMBER: 60/081952  
PROR FILING DATE: 1998-04-15  
PROR APPLICATION NUMBER: 60/081838  
PROR FILING DATE: 1998-04-15  
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PROR FILING DATE: 1998-05-13  
PROR APPLICATION NUMBER: 60/085582  
PROR FILING DATE: 1998-05-15  
PROR APPLICATION NUMBER: 60/085700  
PROR FILING DATE: 1998-05-15  
PROR APPLICATION NUMBER: 60/085689  
PROR FILING DATE: 1998-05-15  
PROR APPLICATION NUMBER: 60/085579  
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PROR FILING DATE: 1998-05-15  
PROR APPLICATION NUMBER: 60/085573  
PROR FILING DATE: 1998-05-15  
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PROR FILING DATE: 1998-05-15  
PROR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;  
Best Local Similarity 99.4%; Pred. No. 3.5e-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSALAGRRGTQAEBSNLSKPFQSSNKEQNGVODPOHERITTVSTNGSIHS 60  
DB 1 MSIFGLLVTSALAGRRGTQAEBSNLSKPFQSSNKEQNGVODPOHERITTVSTNGSIHS 60  
QY 61 PRPHTYPRNTYLVWLVVVEENWVQLTPDERFGLEDEDDICRYDFVEEPPSSGTL 120  
DB 61 PRPHTYPRNTYLVWLVVVEENWVQLTPDERFGLEDEDDICRYDFVEEPPSSGTL 120

QY 121 GRWGSGTVGPGKQISKNQIRIRFVSDYFSPSPGCIHYNIVMPQFTAVSPSULPSPA 180  
Db 121 GRWGSGTVGPGKQISKNQIRIRFVSDYFSPSPGCIHYNIVMPQFTAVSPSULPSPA 180  
QY 181 LPDLNNATATFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNT 240  
Db 181 LPDLNNATATFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNT 240  
QY 241 LTRVRLYSCTRPRNSYSIRELKRDTDTIFWPGCLLYRCCGNCACCLHNCNECQVPSK 300  
Db 241 LTRVRLYSCTRPRNSYSIRELKRDTDTIFWPGCLLYRCCGNCACCLHNCNECQVPSK 300  
QY 301 VTKKHEVLQLRPKTGVRGLHKSITDVALHEHCEDCVCRSGTGG 345  
Db 301 VTKKHEVLQLRPKTGVRGLHKSITDVALHEHCEDCVCRSGTGG 345

RESULT 13  
US-09-978-192A-488  
Sequence 488, Application US/09978192A  
Patent No. US0020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Hillan, Kenneth J.  
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APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
PRIORITY FILING DATE: 2001-10-15  
PRIORITY APPLICATION NUMBER: 09/918585  
PRIORITY FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;  
Best Local Similarity 99.4%; Pred. No. 3, 5e-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MSIFGLLVTSALAGRRGTQAEBSNLSKPPQSSNKEQNGVDPQHERIITVSTNSIS 60  
QY 61 PREPHTYPRNTVYVWVLVVEENWVQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120  
61 PREPHTYPRNTVYVWVLVVEENWVQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120  
DB 61 PREPHTYPRNTVYVWVLVVEENWVQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120  
QY 121 GRWCGSGTVPGKQISKQNOIRIRFVSDEXFPSEPGFCIHNYIMPOFTEAVSPSVLP 180  
121 GRWCGSGTVPGKQISKQNOIRIRFVSDEXFPSEPGFCIHNYIMPOFTEAVSPSVLP 180  
DB 121 GRWCGSGTVPGKQISKQNOIRIRFVSDEXFPSEPGFCIHNYIMPOFTEAVSPSVLP 180  
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181 LPDLNNATITASTIEDIRYLEPFRMQLDEDLRPTWOLGKAFVGRKSRVVDNL 240  
DB 181 LPDLNNATITASTIEDIRYLEPFRMQLDEDLRPTWOLGKAFVGRKSRVVDNL 240  
QY 241 LTFEVRVYSCTPRNFVSIRBELKRTDTIFWPGCLLYKRCGNGACCLHNCECCVPSK 300  
241 LTFEVRVYSCTPRNFVSIRBELKRTDTIFWPGCLLYKRCGNGACCLHNCECCVPSK 300  
DB 241 LTFEVRVYSCTPRNFVSIRBELKRTDTIFWPGCLLYKRCGNGACCLHNCECCVPSK 300  
QY 301 VTKKYHEVLQLRPKTGVRLKSLTDVLEHHEBCDVCRGSTG 345  
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DB 301 VTKKYHEVLQLRPKTGVRLKSLTDVLEHHEBCDVCRGSTG 345  
RESULT 14  
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Sequence 488, Application US/0999832A  
Publication No. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Batton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurley, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999, 832A  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03



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PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 3,5e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSLAAGRGTOAESNLSSKFOFSSNKQNGVDPQHERITTVSTNGSIHS 60
DB 1 MSIFGLLVTSLAAGRGTOAESNLSSKFOFSSNKQNGVDPQHERITTVSTNGSIHS 60
QY 61 PRPHPTPRNTVTLVWRLVAEENWVLIQTFDERPGLDEPDDI CKYDFVEEBSDDTIL 120
DB 61 PRPHPTPRNTVTLVWRLVAEENWVLIQTFDERPGLDEPDDI CKYDFVEEBSDDTIL 120
QY 121 GRWCGSGTVPKQISKQNRIRFVSDPEPSEBPGFCIHYNIVMPQTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKQISKQNRIRFVSDPEPSEBPGFCIHYNIVMPQTEAVSPSVLPSPA 180
QY 181 LPDLNNATTAFTSTEDLIRYLEPEPMQDLEDVLRPTMQLGKAFVFRKSRVVDLNL 240
DB 181 LPDLNNATTAFTSTEDLIRYLEPEPMQDLEDVLRPTMQLGKAFVFRKSRVVDLNL 240
QY 241 LTEEVRVLSCTPRNFVSISIEELKRTTITFMPGCLVYKRCGACACCHNCNCCQCVPSK 300
DB 241 LTEEVRVLSCTPRNFVSISIEELKRTTITFMPGCLVYKRCGACACCHNCNCCQCVPSK 300
QY 301 VTKKYHEVLIQRPRTGVRLGKSLTDVALHHEBCDVCVCGSTGG 345
DB 301 VTKKYHEVLIQRPRTGVRLGKSLTDVALHHEBCDVCVCGSTGG 345

RESULT 15
US-09-978-189-488
Sequence 488, Application US/09978189
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, V. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/083666  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-5-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 10; Length 345;  
Best Local Similarity 99.4%; Pred. No. 3.5e-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 MSPLGLLVTASLAGORGTQAESNLSSKFOFSNKEONGVDPQHRRIITVSTNGSIHS 60  
1 MSPLGLLVTASLAGORGTQAESNLSSKFOFSNKEONGVDPQHRRIITVSTNGSIHS 60  
61 PRPHYTPRNTVLVWRLVAEENVMYIQLTFDERFGLDEPDDICKYDFVEYEESDGTIL 120  
61 PRPHYTPRNTVLVWRLVAEENVMYIQLTFDERFGLDEPDDICKYDFVEYEESDGTIL 120  
121 GRWCGSGTVPGKQSKGNQIRIRFVSDEYPPSESGFCIHNIYVWPOTEAVSPVLPPSA 180  
121 GRWCGSGTVPGKQSKGNQIRIRFVSDEYPPSESGFCIHNIYVWPOTEAVSPVLPPSA 180  
181 LPDLNNATTAFTLBDLRYLEPERWQDLBDLYRPTQLAKAFVFGKSRVVDNL 240  
181 LPDLNNATTAFTLBDLRYLEPERWQDLBDLYRPTQLAKAFVFGKSRVVDNL 240  
241 LTBVRLYSCTPRNFVSISIREBELKRTDTIFWPGCLVRCGNCACCLHNCNECQVPSK 300  
241 LTBVRLYSCTPRNFVSISIREBELKRTDTIFWPGCLVRCGNCACCLHNCNECQVPSK 300  
301 VTKKYHEVLQLRPKTVGRGLHKSITDYALBHEHECQVCVCSGTG 345  
301 VTKKYHEVLQLRPKTVGRGLHKSITDYALBHEHECQVCVCSGTG 345

Search completed: May 27, 2004, 15:56:26  
Job time : 41 secs

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CC ability to stimulate and enhance proliferation or differentiation, and/or  
CC growth or motility of cells expressing a PDGF-C receptor. PDGF-C  
CC polypeptides can be used in pharmaceuticals for promoting cell  
CC proliferation, preferably in combination with one other growth factor and  
CC heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used  
CC for stimulating connective tissue or wound healing. The PDGF-C  
CC polypeptide can be enzymatically processed to generate the active  
CC truncated form of PDGF-C and used to regulate the receptor-binding  
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast  
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.  
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour  
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.  
CC chorioleukemia, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma  
CC and erythroleukemia, can be identified by testing for expression of PDGF-  
CC C. PDGF-C antagonists can also be used to inhibit tissue remodeling  
CC during invasion of tumour cells into a normal population of cells.  
CC Antagonists can also be used to treat fibrotic conditions, especially  
CC found in the lung, kidney or liver

CC Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 3; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4.3e-179; Mismatches 0; Gaps 0;  
Matches 345; Conservative 0; Indels 0;

QY 1 MSIFGLLVTSALAGRRGTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
DB 1 MSIFGLLVTSALAGRRGTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
QY 61 PRPHPTPVNTVYVWRLVAEENWVQLTFDERFGLEDDEDDICXDFVEVEBPSDGTIL 120  
DB 61 PRPHPTPVNTVYVWRLVAEENWVQLTFDERFGLEDDEDDICXDFVEVEBPSDGTIL 120  
QY 121 GRWGSSTGVGKQISGNGQIRIRFVSDPEFSPGFCIHYNIVMPQFTAVSPSVLPESA 180  
DB 121 GRWGSSTGVGKQISGNGQIRIRFVSDPEFSPGFCIHYNIVMPQFTAVSPSVLPESA 180  
QY 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVVDNL 240  
DB 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVVDNL 240  
QY 241 LTBENVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLNCCNCCQVPSK 300  
DB 241 LTBENVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLNCCNCCQVPSK 300  
QY 301 VTKKHYEVQLRPKTGVGRGLHKSITDVALHHEBCDCVCRGSTGG 345  
DB 301 VTKKHYEVQLRPKTGVGRGLHKSITDVALHHEBCDCVCRGSTGG 345

RESULT 2  
AAE13212  
ID AAE13212 standard; protein; 345 AA.

XX AAE13212;  
AC 12-FEB-2002 (first entry)  
DT 12-FEB-2002 (first entry)  
XX Human platelet-derived growth factor (PDGF-C) protein.  
DE Human platelet-derived growth factor (PDGF-C) protein.  
KW Human; transgenic animal; platelet derived growth factor C; PDGF-C;  
KW cardiac hypertrophy; fibrosis.  
XX Homo sapiens.  
OS Homo sapiens.  
PN MO200172132-A1.  
XX 04-OCT-2001.  
PD 04-OCT-2001.  
XX 28-MAR-2001; 2001MO-US009855.  
PF 28-MAR-2001; 2000US-0192507P.  
XX 28-MAR-2000; 2000US-0192507P.  
PR 28-MAR-2000; 2000US-0192507P.  
XX 28-MAR-2000; 2000US-0192507P.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Eriksson U, Li X, Ponten A, Aase K, Li H;

DR WPI; 2002-010700/01.

PT A transgenic animal over-expressing platelet derived growth factor C is  
PT useful to study and find therapy for disease associated with PDGF-C over-  
PT expression, including cardiac hypertrophy and fibrosis.

PS Disclosure; Page 40-42; 48pp; English.

CC The patent discloses a method for producing a transgenic, non-human  
CC animal over-expressing a platelet derived growth factor C (PDGF-C), or  
CC its functional fragment or analogue. The method involves introducing a  
CC transgenic PDGF-C DNA into a cell of a non-human animal, introducing the  
CC cell into a non-human animal and allowing the cell to develop into a  
CC transgenic, non-human animal. The transgenic animal is useful as a model  
CC to study disease states characterised by over-expression of PDGF-C and to  
CC find therapy for those diseases, particularly hypertrophy and fibrosis in  
CC various organs including the heart. The present sequence is PDGF-C  
CC protein from human

SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 5; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4.3e-179; Mismatches 0; Gaps 0;  
Matches 345; Conservative 0; Indels 0;

QY 1 MSIFGLLVTSALAGRRGTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
DB 1 MSIFGLLVTSALAGRRGTQAESNLSSKFOFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
QY 61 PRPHPTPVNTVYVWRLVAEENWVQLTFDERFGLEDDEDDICXDFVEVEBPSDGTIL 120  
DB 61 PRPHPTPVNTVYVWRLVAEENWVQLTFDERFGLEDDEDDICXDFVEVEBPSDGTIL 120  
QY 121 GRWGSSTGVGKQISGNGQIRIRFVSDPEFSPGFCIHYNIVMPQFTAVSPSVLPESA 180  
DB 121 GRWGSSTGVGKQISGNGQIRIRFVSDPEFSPGFCIHYNIVMPQFTAVSPSVLPESA 180  
QY 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVVDNL 240  
DB 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVVDNL 240  
QY 241 LTBENVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLNCCNCCQVPSK 300  
DB 241 LTBENVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLNCCNCCQVPSK 300  
QY 301 VTKKHYEVQLRPKTGVGRGLHKSITDVALHHEBCDCVCRGSTGG 345  
DB 301 VTKKHYEVQLRPKTGVGRGLHKSITDVALHHEBCDCVCRGSTGG 345

RESULT 3  
AA41766  
ID AA41766 standard; protein; 345 AA.

XX AA41766;  
AC 07-DEC-1999 (first entry)  
DT 07-DEC-1999 (first entry)  
XX Human PRO200 protein sequence.  
DE Human PRO200 protein sequence.  
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein.  
XX Homo sapiens.  
OS Homo sapiens.  
PN WO946281-A2.  
XX WO946281-A2.  
PD 16-SEP-1999.  
XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.  
PF  
XX 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077643P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 31-MAR-1998; 98US-0080105P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081239P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0083366P.  
PR 27-APR-1998; 98US-0083368P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083549P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084416P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.

PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-008560P.  
PR 15-MAY-1998; 98US-0085682P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 28-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.

XX (GETH ) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI, 1999-551358/46.

DR N-PSDB; AAZ34296.

XX New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
XX adhesion disorders.

PS Claim 12; Fig 207; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AAZ3891 to AAZ34338, and AAZ41685 to  
CC AAZ41774 represent polynucleotide and polypeptide sequence given in the  
XX exemplification of the present invention

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 2; Length 345;

Best Local Similarity 99.4%; Pred. No. 2,2e-178;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTSBALAGRGTOAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60  
DB 1 MSFLGLLVTSBALAGRGTOAESNLSSKQFSSNKQNGVDPQHERIITVSTNGSIHS 60  
QY PRPHPTPRMTVLVWLRVAABENWVIOITDERGLEDPEDDICKYQFVEVEBPSDGTIL 120  
DB PRPHPTPRMTVLVWLRVAABENWVIOITDERGLEDPEDDICKYQFVEVEBPSDGTIL 120  
QY 61 PRPHPTPRMTVLVWLRVAABENWVIOITDERGLEDPEDDICKYQFVEVEBPSDGTIL 120  
DB 61 PRPHPTPRMTVLVWLRVAABENWVIOITDERGLEDPEDDICKYQFVEVEBPSDGTIL 120  
QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYPSSEBGFCHYNIVMPQFTBAVSPSLPPSA 180  
DB 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYPSSEBGFCHYNIVMPQFTBAVSPSLPPSA 180  
QY 181 LPDLNLNNAITAFSTEDLIRYLEPERWQDLDELYRPTQQLGKAVVFGKRSVVDLNT 240  
DB 181 LPDLNLNNAITAFSTEDLIRYLEPERWQDLDELYRPTQQLGKAVVFGKRSVVDLNT 240  
QY 241 LTBEEVRLYSCTPRRFVSISIREELKRTDTITFMPGCLVYKRCGNCACCLHNCBQCVPYSK 300  
DB 241 LTBEEVRLYSCTPRRFVSISIREELKRTDTITFMPGCLVYKRCGNCACCLHNCBQCVPYSK 300  
QY 301 VTKKYHEVLOLRPTGVRGLHKSLTDVLAHHBECDCVCRGSTGG 345  
DB 301 VTKKYHEVLOLRPTGVRGLHKSLTDVLAHHBECDCVCRGSTGG 345

## RESULT 4

AA30023  
ID AAY30023 standard; protein; 345 AA.

XX  
XX AAY30023;

XX  
XX 11-OCT-1999 (first entry)

XX  
XX Human vascular endothelial growth factor related protein.

DE Vascular endothelial growth factor related protein; VEGF-R protein;  
KM tissue growth inhibition; tumour growth; cancer; tissue growth;  
KM angiogenesis; coronary artery blockage.

XX  
XX Homo sapiens.

XX  
XX MO993671-A1.

XX  
XX 29-JUL-1999.

XX  
XX 26-JAN-1999; 99WO-US001574.

XX  
XX 27-JAN-1998; 98US-0072635P.

XX  
XX 05-JUN-1998; 98US-0080809P.

XX  
XX 24-JUN-1998; 98US-0090544P.

XX  
XX 31-AUG-1998; 98US-0098548P.

XX  
XX (ELIL ) LILLY & CO ELI.

XX  
XX Dou S, Na S, Song HY;

XX  
XX MPI; 1999-458680/38.

XX  
XX N-PSDB; AAX66352.

XX  
XX A vascular endothelial growth factor related protein and related  
XX polynucleotide, useful for identifying antagonists and binding compounds.

XX  
XX Claim 1; Page 56-58; 62pp; English.

CC The present sequence represents a vascular endothelial growth factor  
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify  
CC compounds that bind to it or that antagonize its activity. VEGF-R  
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting  
CC tissue growth. This is useful for inhibiting tumour growth and for  
CC treating cancer. VEGF-R itself can be used to stimulate tissue growth,  
CC angiogenesis and to treat coronary artery blockage. The VEGF-R coding  
CC sequence can be used for the recombinant production of the VEGF-R protein  
XX  
XX  
XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 2; Length 345;

Best Local Similarity 99.4%; Pred. No. 2.2e-178;

Matches 345; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSALAGRGTOAESNLSSKQFSSNKEONGVDPQHERITTVSTNGSIHS 60

DB 1 MSIFGLLVTSALAGRGTOAESNLSSKQFSSNKEONGVDPQHERITTVSTNGSIHS 60

QY 61 PRPHPTVPRNTVAVLRVAEENWVIOITDERPGLDEPDIDICKYDFVEEPPSDGTL 120

DB 61 PRPHPTVPRNTVAVLRVAEENWVIOITDERPGLDEPDIDICKYDFVEEPPSDGTL 120

QY 121 GRGCGSGTVGKQISKGNQIRIRFVSEYSPSEPGCFIHNYIMPOQTEAVSSVLPSPA 180

DB 121 GRGCGSGTVGKQISKGNQIRIRFVSEYSPSEPGCFIHNYIMPOQTEAVSSVLPSPA 180

QY 181 LPLDLNNATTAFTSTLEDLIRYLEPERWQDLDELVRPTWQLGKAFVFGKSRVVDLNL 240

DB 181 LPLDLNNATTAFTSTLEDLIRYLEPERWQDLDELVRPTWQLGKAFVFGKSRVVDLNL 240

QY 241 LITEEVLVSGCTPRNFVSIRBELKRTDTTIFWPGCLLVKRCGNCACCLHNCEQCVPK 300

DB 241 LITEEVLVSGCTPRNFVSIRBELKRTDTTIFWPGCLLVKRCGNCACCLHNCEQCVPK 300

QY 301 VTKKHEVLQLRPKTGVRLHKSITDVALFHHBECDVCVGRSGNG 345

DB 301 VTKKHEVLQLRPKTGVRLHKSITDVALFHHBECDVCVGRSGNG 345

## RESULT 5

AA33679  
ID AAY33679 standard; protein; 345 AA.

XX  
XX AAY33679;

XX  
XX 11-JAN-2000 (first entry)

XX  
XX Human VEGF-E protein.

DE VEGF-E; human; vascular endothelial cell growth factor; wound repair;  
KM treatment; cardiovascular disorder; endothelial disorder; therapy;  
KM tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
KM angiogenic disorder; age-related macular degeneration; vascular disease;  
KM neovascularization; tumor; gene mapping.

XX  
XX Homo sapiens.

XX  
XX MO9947677-A2.

XX  
XX 23-SEP-1999.

XX  
XX 10-MAR-1999; 99WO-US005190.

XX  
XX 17-MAR-1998; 98US-00040220.

XX  
XX 02-NOV-1998; 98US-00184216.

XX  
XX (GETH ) GENENTECH INC.

XX  
XX Ferrara N, Kuo SS,

XX  
XX MPI; 1999-580306/49.

XX  
XX N-PSDB; AAZ23691.

PT New growth factor polypeptide useful for treating cardiovascular or  
PT endothelial disorders, e.g. cardiac hypertrophy.  
XX  
XX Claim 1; Fig 2; 122pp; English.

CC This invention describes the isolation of a novel human vascular  
CC endothelial cell growth factor-E (VEGF-E) polypeptide which has  
CC transinhibitor, vulnery and cardiant activity. VEGF-E can be administered  
CC therapeutically, especially by expressing encoding polynucleotides, to  
CC treat cardiovascular or endothelial disorders in mammals, especially  
CC humans. It is useful in wound repair and tissue generation and  
CC regeneration, and may especially be used to treat cardiac hypertrophy It  
CC can be combined with a carrier in pharmaceutical compositions, which can  
CC be administered to treat disorders as above. VEGF-E can be used to screen  
CC for antagonists and agonists, and the antagonists administered to treat  
CC angiogenic disorders in mammals (especially humans) e.g. cancer or age-  
CC related macular degeneration. It can be used to generate antibodies,  
CC useful therapeutically as antagonists, as above. The antibodies are also  
CC useful to detect VEGF-E polypeptide, especially to diagnose  
CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.  
CC vascular disease, or neovascularization associated with tumor formation),  
CC by contacting the antibody with a tissue sample and detecting formation  
CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-  
CC E can be used to diagnose cardiovascular and endothelial disorders in  
CC mammals, by detecting abnormally high or low VEGF-E gene expression in  
CC tissue samples. They can also be used to diagnose a disease or  
CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a  
CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by  
CC detecting a mutation in the VEGF-E-encoding sequence isolated from a  
CC sample. They may also be used to produce probes useful to detect related  
CC sequences or for gene mapping. This sequence represents the human VEGF-E  
CC protein described in the method of the invention

```

XX      Sequence 345 AA;
SQ      Query Match      99.6%; Score 1851; DB 2; Length 345;
        Best Local Similarity 99.4%; Pred. No. 2.2e-178;
        Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSLLGLLVTALGQRGTQAESLTSKFPSSKKEQNGVDPQHEHITVSTNGSIHS 60
DB      1 MSLLGLLVTALGQRGTQAESLTSKFPSSKKEQNGVDPQHEHITVSTNGSIHS 60
QY      61 PRPHPTVPRNTVLVWRLVAEENWVQLTPDERFGLJEPEDDICKYDFVEYEPSPDGTIL 120
DB      61 PRPHPTVPRNTVLVWRLVAEENWVQLTPDERFGLJEPEDDICKYDFVEYEPSPDGTIL 120
QY      61 PRPHPTVPRNTVLVWRLVAEENWVQLTPDERFGLJEPEDDICKYDFVEYEPSPDGTIL 120
DB      61 PRPHPTVPRNTVLVWRLVAEENWVQLTPDERFGLJEPEDDICKYDFVEYEPSPDGTIL 120
QY      121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHVNIWVQFTEAVSPSVLPSPA 180
DB      121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHVNIWVQFTEAVSPSVLPSPA 180
QY      121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHVNIWVQFTEAVSPSVLPSPA 180
DB      121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHVNIWVQFTEAVSPSVLPSPA 180
QY      181 LPLDLNNATAFSTLEDLIRYLBPERWQLEDLYRFTWQLGKAFVFGKRSRVVDINTL 240
DB      181 LPLDLNNATAFSTLEDLIRYLBPERWQLEDLYRFTWQLGKAFVFGKRSRVVDINTL 240
QY      241 LTBEEVRLVSCTPRNFVSISIRELAKRTDTIFWPGCLVRCGNCACCLHNCNCCQVPSK 300
DB      241 LTBEEVRLVSCTPRNFVSISIRELAKRTDTIFWPGCLVRCGNCACCLHNCNCCQVPSK 300
QY      301 VTKKYHEVQLRPKTGVRLHKSITDVALHEHBECDVCYCRGSTGG 345
DB      301 VTKKYHEVQLRPKTGVRLHKSITDVALHEHBECDVCYCRGSTGG 345

RESULT 6
AAB33414
ID      AAB33414 standard; protein; 345 AA.
AC      AAB33414;
XX      29-JAN-2001 (first entry)
XX      Human PRO200 protein UNQ174 SEQ ID NO:2.
DE      Human; immune related disease; diagnosis; anti-inflammatory; cardiac;
KW      dermatological; antidiabetic; antirheumatic; immunosuppressive;
KW      haemostatic; antithyroid; antidiabetic; neuroprotective;
KW      antiautismic; hepatic; virucide; antiparasitic; antiallergic;
KW      osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;
KW      idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW      systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW      autoimmune thrombocytopenia; immune-mediated renal disease;
KW      demyelinating disease; hepatobiliary disease; Whipple's disease;
KW      inflammatory bowel disease; gluten-sensitive enteropathy;
KW      autoimmune disease; immune-mediated skin disease; allergic disease;
KW      immunological disease; transplantation associated disease;
KW      graft rejection; graft-versus-host-disease.
XX      Homo sapiens.
OS      Homo sapiens.
XX      MO200053758-A2.
XX      14-SEP-2000.
XX      02-MAR-2000; 2000WO-US005841.
XX      08-MAR-1999; 99WO-US005028.
XX      10-MAR-1999; 99US-0123618P.
XX      12-MAR-1999; 99US-0123957P.
XX      23-MAR-1999; 99US-0125775P.
XX      12-APR-1999; 99US-0128849P.
XX      20-APR-1999; 99WO-US008615.
XX      28-APR-1999; 99US-0131445P.
XX      04-MAY-1999; 99US-0132371P.

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PR      14-MAY-1999; 99US-0134287P.
PR      02-JUN-1999; 99WO-US012252.
PR      23-JUN-1999; 99US-0141037P.
PR      20-JUL-1999; 99US-0144758P.
PR      26-JUL-1999; 99US-0145698P.
PR      28-JUL-1999; 99US-0146222P.
PR      01-SEP-1999; 99WO-US020111.
PR      08-SEP-1999; 99WO-US020594.
PR      13-SEP-1999; 99WO-US020944.
PR      15-SEP-1999; 99WO-US021090.
PR      15-SEP-1999; 99WO-US021547.
PR      05-OCT-1999; 99WO-US023089.
PR      29-OCT-1999; 99US-0162506P.
PR      29-NOV-1999; 99WO-US028214.
PR      30-NOV-1999; 99WO-US028313.
PR      30-NOV-1999; 99WO-US028409.
PR      01-DEC-1999; 99WO-US028301.
PR      01-DEC-1999; 99WO-US028634.
PR      02-DEC-1999; 99WO-US028551.
PR      02-DEC-1999; 99WO-US028564.
PR      02-DEC-1999; 99WO-US028565.
PR      16-DEC-1999; 99WO-US030095.
PR      20-DEC-1999; 99WO-US030999.
PR      30-DEC-1999; 99WO-US031274.
PR      05-JAN-2000; 2000WO-US000219.
PR      06-JAN-2000; 2000WO-US000277.
PR      11-FEB-2000; 2000WO-US000376.
PR      11-FEB-2000; 2000WO-US003565.
PR      18-FEB-2000; 2000WO-US004341.
PR      18-FEB-2000; 2000WO-US004342.
PR      22-FEB-2000; 2000WO-US004414.

XX      (GETH ) GENENTECH INC.
XX      Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
XX      Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
XX      Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX      WPI; 2000-572271/53.
XX      N-PSDB; AAC58579.
XX      Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX      immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX      arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX      Claim 33; Fig 2; 309pp; English.
XX      The present invention describes sixty four human PRO proteins which can
XX      be used in the treatment of immune related diseases. The human PRO
XX      proteins, anti-PRO antibodies, agonists and antagonists are useful for
XX      treating and diagnosing immune related disorders. The disorders are
XX      selected from systemic lupus erythematosus, rheumatoid arthritis,
XX      osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX      systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX      syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX      anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
XX      immune-mediated renal disease, demyelinating diseases of the central and
XX      peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
XX      disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
XX      or immune-mediated skin diseases, allergic diseases, immunological
XX      diseases of the lung, and transplantation associated diseases including
XX      graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
XX      represent PCR primers and hybridisation probes used in the isolation of
XX      human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
XX      represent human PRO polynucleotide and protein sequences given in the
XX      exemplification of the present invention
SQ      Sequence 345 AA;

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Query Match      99.6%; Score 1851; DB 3; Length 345;
Best Local Similarity 99.4%; Pred. No. 2.2e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSIFGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERIITVSTNGSIHS 60  
 DB 1 MSIFGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERIITVSTNGSIHS 60  
 QY 61 PREPHYTPNTVLMVLAEEVENVWLTQTFDERFGLEDDEDDICKDFVEVEEPPSGITLL 120  
 DB 61 PREPHYTPNTVLMVLAEEVENVWLTQTFDERFGLEDDEDDICKDFVEVEEPPSGITLL 120  
 QY 121 GRWCGSGTVPKQOISKGNQIRIRFVSDPEPSEPGFCIHNYIMPOFTEAVSSVLPSPA 180  
 DB 121 GRWCGSGTVPKQOISKGNQIRIRFVSDPEPSEPGFCIHNYIMPOFTEAVSSVLPSPA 180  
 QY 181 LPDLNNMNTAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNL 240  
 DB 181 LPDLNNMNTAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNL 240  
 QY 241 LTFEVRVLYSCTPRNFVSIRBELKRTDTTFWPGCLLYKRCGGNACCLHNCNCCQVPSK 300  
 DB 241 LTFEVRVLYSCTPRNFVSIRBELKRTDTTFWPGCLLYKRCGGNACCLHNCNCCQVPSK 300  
 QY 301 VTKKYEVLQLRPKTGVRLGKSLTDVALHHEHBCDCVCRGSGTG 345  
 DB 301 VTKKYEVLQLRPKTGVRLGKSLTDVALHHEHBCDCVCRGSGTG 345

RESULT 7  
 AAB19578  
 ID AAB19578 standard; protein; 345 AA.  
 AC AAB19578;  
 XX  
 DT 22-JAN-2001 (first entry)  
 DE Human PRO200 (vascular endothelial growth factor B).  
 XX  
 KW PRO200; vascular epithelial growth factor B; VEGF-E; human;  
 KW ocular disease; retinopathy; maculopathy; therapy; retinitis pigmentosa;  
 KW macular degeneration; retinal detachment; retinal tear; macular hole;  
 KW myopia; traumatic choriorretinopathy; acute retinal necrosis syndrome;  
 KW contusion; edema; retinal vision occlusion; vascular disease;  
 KW retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..14  
 FT /label= Signal\_peptide  
 FT Protein 15..345  
 FT /label= Mature\_Pro200  
 FT Modified-site 15..21  
 FT /note= "N-myristoylation"  
 FT Modified-site 25..29  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 55..59  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 117..123  
 FT /note= "N-myristoylation"  
 FT Modified-site 127..133  
 FT /note= "N-myristoylation"  
 FT Modified-site 254..258  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 281..287  
 FT /note= "N-myristoylation"  
 FT Modified-site 282..288  
 FT /note= "N-myristoylation"  
 FT Modified-site 319..325  
 FT /note= "Amidation"  
 XX  
 PN WO20053760-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 10-MAR-2000; 2000MO-US006319.

XX 12-MAR-1999; 99US-0123957P.  
 XX  
 XX (GENTECH) INC.  
 PA Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ,  
 PI Kabakoff RC, Klein RD, Kljavin ID, Kuo SS, La Fleur M, Wood WI;  
 XX WPI: 2000-587437/55.  
 DR N-PSDB: AAA88515.  
 XX  
 PT Novel PRO polypeptides useful for preventing or rescuing retinal cells  
 PT from injury caused by ocular diseases such as retinitis pigmentosa,  
 PT retinopathy, retinal degenerative diseases, degenerative myopia, uveitis.  
 XX  
 PS Claim 2; Fig 2; 140pp; English.  
 CC  
 CC The present sequence is that of human PRO200 or vascular endothelial  
 CC growth factor B (VEGF-B), as predicted from a cDNA clone (see AAA88515)  
 CC that was isolated from a glioma cell line G61 library using probes (see  
 CC AAA88523-26) based on an expressed sequence tag (see AAA88522) that  
 CC showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a  
 CC pI of about 6.06. A method for producing PRO polypeptides, including  
 CC PRO200, using a host cell transformed with a vector comprising a PRO  
 CC nucleic acid is claimed. The invention relates to the use of PRO  
 CC polypeptides to delay, prevent or rescue retinal cells such as retinal  
 CC neurons selected from photoreceptors, retinal ganglion cells, displaced  
 CC retinal ganglion cells, amacrine cells, displaced amacrine cells,  
 CC horizontal and bipolar neurons, and supportive cells (including Mueller  
 CC cells and pigment epithelial cells) from injury and degeneration. The  
 CC retinal cells are preferably photoreceptors and photoreceptor cell injury  
 CC or death is caused by retinal injury, light or environmental trauma or by  
 CC an ocular disease selected from retinitis pigmentosa, macular  
 CC degeneration, including age-related, retinal detachment, retinal tears,  
 CC retinopathy, retinal degenerative diseases, macular holes, degenerative  
 CC myopia, acute retinal necrosis syndrome, traumatic choriorretinopathies or  
 CC contusion such as Purtscher's retinopathy, edema, ischemic conditions  
 CC such as central or branch retinal vision occlusion, collagen vascular  
 CC diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and  
 CC occlusion associated with Bales disease and systemic lupus erythematosus  
 CC (claimed)  
 CC  
 XX  
 SQ Sequence 345 AA;  
 Query Match 99.6%; Score 1851; DB 3; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSIFGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERIITVSTNGSIHS 60  
 DB 1 MSIFGLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHERIITVSTNGSIHS 60  
 QY 61 PREPHYTPNTVLMVLAEEVENVWLTQTFDERFGLEDDEDDICKDFVEVEEPPSGITLL 120  
 DB 61 PREPHYTPNTVLMVLAEEVENVWLTQTFDERFGLEDDEDDICKDFVEVEEPPSGITLL 120  
 QY 121 GRWCGSGTVPKQOISKGNQIRIRFVSDPEPSEPGFCIHNYIMPOFTEAVSSVLPSPA 180  
 DB 121 GRWCGSGTVPKQOISKGNQIRIRFVSDPEPSEPGFCIHNYIMPOFTEAVSSVLPSPA 180  
 QY 181 LPDLNNMNTAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNL 240  
 DB 181 LPDLNNMNTAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDLNL 240  
 QY 241 LTFEVRVLYSCTPRNFVSIRBELKRTDTTFWPGCLLYKRCGGNACCLHNCNCCQVPSK 300  
 DB 241 LTFEVRVLYSCTPRNFVSIRBELKRTDTTFWPGCLLYKRCGGNACCLHNCNCCQVPSK 300  
 QY 301 VTKKYEVLQLRPKTGVRLGKSLTDVALHHEHBCDCVCRGSGTG 345  
 DB 301 VTKKYEVLQLRPKTGVRLGKSLTDVALHHEHBCDCVCRGSGTG 345



RESULT 8  
AAB10651  
ID AAB10651 standard; protein: 345 AA.  
XX  
AC AAB10651;  
XX  
DT 19-JAN-2001 (first entry)  
XX  
DE Human VEGF-X protein #3.  
XX  
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytoskeletal;  
KW antiinflammatory; antiarthritic; antipapillary; antidiabetic; treatment;  
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
KW venous sore; diabetic ulcer; burns; skin graft growth.  
XX  
OS Homo sapiens.  
XX  
PN WO200037641-A2.  
XX  
PD 29-JUN-2000.  
XX  
PF 21-DEC-1999; 99WO-US030503.  
XX  
PR 22-DEC-1998; 98GB-00028377.  
PR 18-MAR-1999; 99US-0124967P.  
PR 08-NOV-1999; 99US-0164131P.  
XX  
PA (JANNC ) JANSSEN PHARM NV.  
XX  
PI Gordon RD, Sprengel JT, Yon JR, Dijkman JH, Gostewska A;  
PI Dhanaaraj SN, Xu J;  
XX  
DR WPI: 2000-442669/38.  
XX  
PT New vascular endothelial growth factor protein, useful for treating or  
PT preventing diseases associated with inappropriate angiogenesis activity  
PT such as cancer, rheumatoid arthritis, psoriasis and wounds.  
XX  
PS Claim 72; Fig 12; 127pp; English.  
XX  
CC This invention describes a novel vascular endothelial growth factor-X  
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
CC vulnery, cytoskeletal, antiinflammatory, antiarthritic, antipapillary and  
CC antidiabetic activity and acts as an angiogenesis and vascularization  
CC regulator. An antisense molecule of the invention is useful for treating  
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
CC retinopathy by inhibiting angiogenic activity or inappropriate  
CC vascularization including formation and proliferation of new blood  
CC vessels, growth and development of tissues, tissue regeneration and organ  
CC and tissue repair in a subject. The products of the invention are useful  
CC for preparing medicaments for treating wounds such as dermal ulcers,  
CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
CC skin graft growth, tissue repair, proliferation of new blood vessels,  
CC tissue regeneration and organ repair by promoting angiogenic activity or  
CC vascularization. This sequence represents the human VEGF-X protein  
CC described in the method of the invention  
XX  
SQ Sequence 345 AA;  
Query Match 99.6%; Score 1851; DB 3; Length 345;  
Best Local Similarity 99.4%; Pred. No. 2.2e-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MSLLGLLTVTSALAGRRGTQAESNLSSKPFSSNKEONGVODPOHERIITVTSNGSIHS 60  
DB 1 MSLLGLLTVTSALAGRRGTQAESNLSSKPFSSNKEONGVODPOHERIITVTSNGSIHS 60  
OY 61 PRPHPTVPRNTVTLVWRLVAEENWVIOITFDERFGLBDEDDICKYDFVEVEPSDGTIL 120  
DB 61 PRPHPTVPRNTVTLVWRLVAEENWVIOITFDERFGLBDEDDICKYDFVEVEPSDGTIL 120

RESULT 9  
AAB10633  
ID AAB10633 standard; protein: 345 AA.  
XX  
AC AAB10633;  
XX  
DT 19-JAN-2001 (first entry)  
XX  
DE Human RACE generated VEGF-X protein.  
XX  
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytoskeletal;  
KW antiinflammatory; antiarthritic; antipapillary; antidiabetic; treatment;  
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
KW venous sore; diabetic ulcer; burns; skin graft growth.  
XX  
OS Homo sapiens.  
XX  
PN WO200037641-A2.  
XX  
PD 29-JUN-2000.  
XX  
PF 21-DEC-1999; 99WO-US030503.  
XX  
PR 22-DEC-1998; 98GB-00028377.  
PR 18-MAR-1999; 99US-0124967P.  
PR 08-NOV-1999; 99US-0164131P.  
XX  
PA (JANNC ) JANSSEN PHARM NV.  
XX  
PI Gordon RD, Sprengel JT, Yon JR, Dijkman JH, Gostewska A;  
PI Dhanaaraj SN, Xu J;  
XX  
DR WPI: 2000-442669/38.  
XX  
PT New vascular endothelial growth factor protein, useful for treating or  
PT preventing diseases associated with inappropriate angiogenesis activity  
PT such as cancer, rheumatoid arthritis, psoriasis and wounds.  
XX  
PS Disclosure; Fig 6; 127pp; English.  
XX  
CC This invention describes a novel vascular endothelial growth factor-X  
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
CC vulnery, cytoskeletal, antiinflammatory, antiarthritic, antipapillary and  
CC antidiabetic activity and acts as an angiogenesis and vascularization  
CC regulator. An antisense molecule of the invention is useful for treating  
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
CC retinopathy by inhibiting angiogenic activity or inappropriate  
CC vascularization including formation and proliferation of new blood  
CC vessels, growth and development of tissues, tissue regeneration and organ  
CC and tissue repair in a subject. The products of the invention are useful  
CC for preparing medicaments for treating wounds such as dermal ulcers,  
CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the RACE generated human VEGF-X  
 CC protein described in the method of the invention  
 XX

SO Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLGILLTSAAGRGQAGQASNLSSKQFSSNKEQNGVDPQHERITVTSTNGSIHS 60  
 DB 1 MSLLGILLTSAAGRGQAGQASNLSSKQFSSNKEQNGVDPQHERITVTSTNGSIHS 60  
 QY 61 PRPHPTPRNTVLVWRLVAEENWVWLTQTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120  
 DB 61 PRPHPTPRNTVLVWRLVAEENWVWLTQTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120  
 QY 121 GRWCGSGTVPQKQISKGNQIRIRFVSDYFPSPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 DB 121 GRWCGSGTVPQKQISKGNQIRIRFVSDYFPSPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 QY 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELVPWQLGKAFVGRKSRVVDNL 240  
 DB 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELVPWQLGKAFVGRKSRVVDNL 240  
 QY 241 LTEEVLVYCTPPNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCCNCCQCVPSK 300  
 DB 241 LTEEVLVYCTPPNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCCNCCQCVPSK 300  
 QY 301 VTKKHEVTLQRPKTGVRLHKSITDVALHHEBCDCVCRGSTGG 345  
 DB 301 VTKKHEVTLQRPKTGVRLHKSITDVALHHEBCDCVCRGSTGG 345

# RESULT 10

AAB10650 ID AAB10650 standard; protein; 345 AA.

XX AAB10650;

DT 19-JAN-2001 (first entry)

XX Human 990126vegX protein.

DE VEGF-X; vascular endothelial growth factor; human; vulnery; cyostatic;  
 XX antiinflammatory; antiatherosclerotic; antidiabetic; treatment;  
 KM angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KM rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KM tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KM venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

OS WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US030503.

XX 22-DEC-1998; 98GB-00028377.

XX 18-MAR-1999; 99US-0124967P.

XX 08-NOV-1999; 99US-0164131P.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

XX Dhanraj SN, Xu J;

XX WPI; 2000-442669/38.

PT New vascular endothelial growth factor protein, useful for treating or  
 preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds.  
 XX Disclosure; Fig 11, 127pp; English.

CC This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (1a) and its encoding polynucleotide (1a) which has  
 CC vulnery, cyostatic, antiatherosclerotic, antidiabetic, antiproliferative and  
 CC antiinflammatory activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the human 990126vegX protein  
 CC used to illustrate the method of the invention

SO Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 3; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLGILLTSAAGRGQAGQASNLSSKQFSSNKEQNGVDPQHERITVTSTNGSIHS 60  
 DB 1 MSLLGILLTSAAGRGQAGQASNLSSKQFSSNKEQNGVDPQHERITVTSTNGSIHS 60  
 QY 61 PRPHPTPRNTVLVWRLVAEENWVWLTQTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120  
 DB 61 PRPHPTPRNTVLVWRLVAEENWVWLTQTFDERFGLEDPEDDICKYDFVEEPPSDGTL 120  
 QY 121 GRWCGSGTVPQKQISKGNQIRIRFVSDYFPSPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 DB 121 GRWCGSGTVPQKQISKGNQIRIRFVSDYFPSPGFCIHYNIVMPQFTEAVSPSVLPSSA 180  
 QY 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELVPWQLGKAFVGRKSRVVDNL 240  
 DB 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELVPWQLGKAFVGRKSRVVDNL 240  
 QY 241 LTEEVLVYCTPPNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCCNCCQCVPSK 300  
 DB 241 LTEEVLVYCTPPNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCCNCCQCVPSK 300  
 QY 301 VTKKHEVTLQRPKTGVRLHKSITDVALHHEBCDCVCRGSTGG 345  
 DB 301 VTKKHEVTLQRPKTGVRLHKSITDVALHHEBCDCVCRGSTGG 345

# RESULT 11

AAB10635 ID AAB10635 standard; protein; 345 AA.

XX AAB10635;

DT 19-JAN-2001 (first entry)

XX Human VEGF-X protein #1 isolated from clones 4 and 7.

DE VEGF-X; vascular endothelial growth factor; human; vulnery; cyostatic;  
 XX antiinflammatory; antiatherosclerotic; antidiabetic; treatment;  
 KM angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KM rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KM tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KM venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

XX WO200037641-A2.

XX

PD 29-JUN-2000.  
 XX 21-DEC-1999; 99WO-US030503.  
 PF 22-DEC-1998; 98GB-00028377.  
 PR 18-MAR-1999; 99US-0124967P.  
 PR 08-NOV-1999; 99US-0164131P.  
 XX (JANC ) JANSSEN PHARM NV.  
 PA Gordon RD, Sprengel JI, Yon JR, Dijkmane JH, Gosiowska A;  
 PI Dhanaraj SN, Xu J;  
 XX WPI: 2000-442669/38.  
 DR N-PSDB; AAA71955.  
 XX New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds.  
 XX  
 PS Disclosure; Fig 9; 127pp; English.  
 XX This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
 CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the human VEGF-X protein  
 CC isolated from clones 4 and 7 described in the method of the invention  
 XX  
 XX Sequence 345 AA;  
 SQ  
 Query Match 99.6%; Score 1851; DB 3; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSLFGLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 DB 1 MSLFGLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 QY 61 PRPHITPRNTVWLRVAVAEENWIOITDERFGLDEPDDICKYDFVEEBSDDGTL 120  
 DB 61 PRPHITPRNTVWLRVAVAEENWIOITDERFGLDEPDDICKYDFVEEBSDDGTL 120  
 QY 121 GRMGSGTVPQKQSKGNQIRIRFVSDYFPESEPGFCHINIVMPQFTEAVSPVLPESA 180  
 DB 121 GRMGSGTVPQKQSKGNQIRIRFVSDYFPESEPGFCHINIVMPQFTEAVSPVLPESA 180  
 QY 181 LPLDLLNNAITAFSTLEDLIRYLBEPWQDLDELIRPTWQLGKAFVFGKSRVVDLNT 240  
 DB 181 LPLDLLNNAITAFSTLEDLIRYLBEPWQDLDELIRPTWQLGKAFVFGKSRVVDLNT 240  
 QY 241 LTBVRLVYSCTPRPFVSISREBELKRTDTIIMPGLIVRCGNCACCLANECOCVPSK 300  
 DB 241 LTBVRLVYSCTPRPFVSISREBELKRTDTIIMPGLIVRCGNCACCLANECOCVPSK 300  
 QY 301 VTKKYHEVLQLRPKTVGRLAKSLTDVALLEHNEBCDCVCRSGTSG 345  
 DB 301 VTKKYHEVLQLRPKTVGRLAKSLTDVALLEHNEBCDCVCRSGTSG 345

RESULT 12  
 AAB10644  
 ID AAB10644 standard; protein; 345 AA.

XX AAB10644;  
 AC 19-JAN-2001 (first entry)  
 DT Human VEGF-X protein #4.  
 DE VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;  
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200037641-A2.  
 XX 29-JUN-2000.  
 PD 21-DEC-1999; 99WO-US030503.  
 PF 22-DEC-1998; 98GB-00028377.  
 PR 18-MAR-1999; 99US-0124967P.  
 PR 08-NOV-1999; 99US-0164131P.  
 XX (JANC ) JANSSEN PHARM NV.  
 PA Gordon RD, Sprengel JI, Yon JR, Dijkmane JH, Gosiowska A;  
 PI Dhanaraj SN, Xu J;  
 XX WPI: 2000-442669/38.  
 DR N-PSDB; AAA71950.  
 XX New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds.  
 XX  
 XX Disclosure; Fig 30B; 127pp; English.  
 XX This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
 CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents a human VEGF-X protein  
 CC described in the method of the invention  
 XX  
 XX Sequence 345 AA;  
 SQ  
 Query Match 99.6%; Score 1851; DB 3; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSLFGLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 DB 1 MSLFGLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
 QY 61 PRPHITPRNTVWLRVAVAEENWIOITDERFGLDEPDDICKYDFVEEBSDDGTL 120  
 DB 61 PRPHITPRNTVWLRVAVAEENWIOITDERFGLDEPDDICKYDFVEEBSDDGTL 120  
 QY 121 GRMGSGTVPQKQSKGNQIRIRFVSDYFPESEPGFCHINIVMPQFTEAVSPVLPESA 180  
 DB 121 GRMGSGTVPQKQSKGNQIRIRFVSDYFPESEPGFCHINIVMPQFTEAVSPVLPESA 180

Db 121 GRWCGSGTVPGKQISKGNQIRFVSDRYPSSEPGFCIHNIIVMPQFTEAVSPVLPPSA 180  
 Qy 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELRYPTWQGLKAFVFGKRSVVDLNL 240  
 Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELRYPTWQGLKAFVFGKRSVVDLNL 240  
 Qy 241 LITEVRLYSCTPRNFSVSIREBELKRTDTTFWPGCLVYKRCGACCLHNCNECCVPSK 300  
 Db 241 LITEVRLYSCTPRNFSVSIREBELKRTDTTFWPGCLVYKRCGACCLHNCNECCVPSK 300  
 Qy 301 VTKKHYEVLQLRPKTGVKGLHKSLLTDVALHHEBECDCVCGSTGG 345  
 Db 301 VTKKHYEVLQLRPKTGVKGLHKSLLTDVALHHEBECDCVCGSTGG 345

RESULT 13  
 AAB44322  
 ID AAB44322 standard; protein, 345 AA.  
 AC AAB44322;  
 XX 08-FEB-2001 (first entry)  
 DT  
 XX Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.  
 KM Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;  
 KW expressed sequence tag; detection; cancer.  
 XX Homo sapiens.  
 OS  
 PN WO200053756-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-US004341.  
 XX  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 29-MAR-1999; 99US-0126773P.  
 PR 21-APR-1999; 99US-0130232P.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US028565.  
 PR 30-DEC-1999; 99WO-US030095.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 05-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000279.  
 PR 06-JAN-2000; 2000WO-US000376.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Flyvareff E, Fong S, Gao W, Gelber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
 PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX  
 DR WPI; 2000-611443/58.  
 DR N-PSDB; AAC78582.  
 XX  
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to  
 PT target bioactive molecules to specific cells, and to modulate cellular  
 PT activities.  
 PS Claim 12; Fig 207; 636DP; English.  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence

CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
 CC The PRO polynucleotides and polypeptides have cytosolic activity. The  
 CC polynucleotides and polypeptides can be used for detecting the presence  
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
 CC and for modulating biological activities of cells, using the polypeptides  
 CC for specific targeting. The polypeptide targeting can be used to kill the  
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
 CC AAC78987 represent PCR primers and probes used in the isolation of the  
 CC PRO polynucleotide sequences  
 CC  
 SQ Sequence 345 AA;  
 XX

Query Match 99.6%; Score 1851; DB 3; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 2,2e-178;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFLGLLVTSAAGRGTOAESNLSSKQFSSSNKEQNGVDPQHRITTVSTNGSIHS 60  
 Db 1 MSFLGLLVTSAAGRGTOAESNLSSKQFSSSNKEQNGVDPQHRITTVSTNGSIHS 60  
 Qy 61 PREPHYPRNTVAVWRLVAEENWVQLTFDERFGLDEPDDICXDPFVVEBPSDGL 120  
 Db 61 PREPHYPRNTVAVWRLVAEENWVQLTFDERFGLDEPDDICXDPFVVEBPSDGL 120  
 Qy 121 GRWCGSGTVPGKQISKGNQIRFVSDRYPSSEPGFCIHNIIVMPQFTEAVSPVLPPSA 180  
 Db 121 GRWCGSGTVPGKQISKGNQIRFVSDRYPSSEPGFCIHNIIVMPQFTEAVSPVLPPSA 180  
 Qy 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELRYPTWQGLKAFVFGKRSVVDLNL 240  
 Db 181 LPDLNNATTAFTSTEDLIRYLEPERWQDLDELRYPTWQGLKAFVFGKRSVVDLNL 240  
 Qy 241 LITEVRLYSCTPRNFSVSIREBELKRTDTTFWPGCLVYKRCGACCLHNCNECCVPSK 300  
 Db 241 LITEVRLYSCTPRNFSVSIREBELKRTDTTFWPGCLVYKRCGACCLHNCNECCVPSK 300  
 Qy 301 VTKKHYEVLQLRPKTGVKGLHKSLLTDVALHHEBECDCVCGSTGG 345  
 Db 301 VTKKHYEVLQLRPKTGVKGLHKSLLTDVALHHEBECDCVCGSTGG 345

RESULT 14  
 AAB24412  
 ID AAB24412 standard; protein, 345 AA.  
 AC AAB24412;  
 XX 07-NOV-2000 (first entry)  
 DT  
 XX Human PRO713 protein sequence SEQ ID NO:137.  
 KM Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiac; cardiovascular; antithrombotic;  
 KW cytosolic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US028313.  
 XX  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 16-DEC-1998; 98US-0112850P.  
 PR 12-JAN-1999; 99US-0115549P.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 02-JUN-1999; 99WO-US012252.

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PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Garber H, Hillan KJ,
XX Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF,
XX Smith V, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2000-412154/35.
XX N-PSDB; AAA77621.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
XX FT and treating diagnosing a cardiovascular, endothelial or angiogenic
XX FT disorders in mammals.
XX
XX Claim 72; Fig 50; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
XX CC useful for preventing, diagnosing and treating diagnosing a
XX CC cardiovascular, endothelial or angiogenic disorder in mammals by
XX CC modulating cell proliferation, angiogenesis and cardiovascularization,
XX CC and for identifying agonists and antagonists of these processes. The
XX CC nucleic acids and the proteins they encode may be used in the prevention,
XX CC treatment and diagnosis of diseases associated with inappropriate PRO
XX CC expression such as cardiovascular, endothelial or angiogenic disorders in
XX CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
XX CC example, the nucleic acids (NCs) and vectors containing them and the PRO
XX CC polypeptide may be used to treat disorders associated with decreased PRO
XX CC expression. AAA77510 to AAA77721 and AAA24388 to AAA24435 represent
XX CC nucleotide and protein sequences used in the exemplification of the
XX CC present invention
XX
XX Sequence 345 AA;
XX
XX Query Match 99.6%; Score 1851; DB 3; Length 345;
XX Best Local Similarity 99.4%; Pred. No. 2.2e-178;
XX Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MSFLGLLVTSALAGRRGTOAESNLSSKPFQSSNKEONGYODPOHERITVSTNGSIHS 60
QY 1 MSFLGLLVTSALAGRRGTOAESNLSSKPFQSSNKEONGYODPOHERITVSTNGSIHS 60
Db 1 MSFLGLLVTSALAGRRGTOAESNLSSKPFQSSNKEONGYODPOHERITVSTNGSIHS 60
QY 61 PRPHPTVPRNTVLVWRVAVENWVQLTFDERFGLDEDDICKYDFVAVEBPDGITL 120
QY 61 PRPHPTVPRNTVLVWRVAVENWVQLTFDERFGLDEDDICKYDFVAVEBPDGITL 120
Db 61 PRPHPTVPRNTVLVWRVAVENWVQLTFDERFGLDEDDICKYDFVAVEBPDGITL 120
QY 121 GRMGSGVPRKQISKGNQIRIRFVSDYFPSEBPCFHNYIWMQFTEAVSPVLPESA 180
QY 121 GRMGSGVPRKQISKGNQIRIRFVSDYFPSEBPCFHNYIWMQFTEAVSPVLPESA 180
Db 121 GRMGSGVPRKQISKGNQIRIRFVSDYFPSEBPCFHNYIWMQFTEAVSPVLPESA 180
QY 181 LPDLNNATAFSTLEDLIRYLBEPWQLDLEDYRPTWOLGKAFVFGKSRVVDNTL 240
QY 181 LPDLNNATAFSTLEDLIRYLBEPWQLDLEDYRPTWOLGKAFVFGKSRVVDNTL 240
Db 181 LPDLNNATAFSTLEDLIRYLBEPWQLDLEDYRPTWOLGKAFVFGKSRVVDNTL 240
QY 241 LTBEEVRLVSCPRNFVSISREELKRTDTIIPMGCLVVRGCGNACCLHNCNCCQVPSK 300
QY 241 LTBEEVRLVSCPRNFVSISREELKRTDTIIPMGCLVVRGCGNACCLHNCNCCQVPSK 300
Db 241 LTBEEVRLVSCPRNFVSISREELKRTDTIIPMGCLVVRGCGNACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGGLKSLTDVALHEHBECDVCRCSTGG 345
QY 301 VTKKYHEVLQLRPKTVGGLKSLTDVALHEHBECDVCRCSTGG 345
Db 301 VTKKYHEVLQLRPKTVGGLKSLTDVALHEHBECDVCRCSTGG 345

```

RESULT 15

```

AAV59285
ID AAV59285 standard; protein; 345 AA.
XX
XX AAV59285;
AC
XX 25-APR-2000 (first entry)
DT
XX
XX Bone morphogenic protein (BMP) (clone HETAB62).
XX
XX Bone morphogenic protein; BMP; cytotactic; osteopathic; angiogenic;
XX KW vulnery; bone disorder; osteoarthritis; cartilage defect; human;
XX tissue repair; gene therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..22
XX FT /note= "signal peptide"
XX FT Peptide 15..26
XX FT /note= "immunogenic epitope"
XX FT Protein 23..345
XX FT /note= "mature protein"
XX FT Peptide 33..46
XX FT /note= "immunogenic epitope"
XX FT Peptide 133..138
XX FT /note= "immunogenic epitope"
XX FT Peptide 214..220
XX FT /note= "immunogenic epitope"
XX FT Peptide 249..255
XX FT /note= "immunogenic epitope"
XX FT Peptide 261..267
XX FT /note= "immunogenic epitope"
XX
XX WO200004183-A1.
XX
XX 27-JAN-2000.
XX
XX 14-JUL-1999; 99WO-US015783.
XX
XX 15-JUL-1998; 98US-0092922P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Young PE;
XX WPI; 2000-182442/16.
XX N-PSDB; AAZ48599.
XX
XX Novel cDNA encoding human bone morphogenic proteins, vectors, host cells
XX FT and methods of recombinant production, useful for diagnosis and treatment
XX FT of, e.g. bone disorders.
XX
XX Claim 11; Page 183-184; 187pp; English.
XX
XX The invention provides novel human bone morphogenic proteins (BMP) and
XX CC nucleic acids encoding the BMPs. The BMP polypeptides can be expressed by
XX CC standard recombinant methodology. Determining the presence or absence of
XX CC a mutation in the polynucleotides or determining the presence or amount
XX CC of expression of the polynucleotides is useful for diagnosing a pathological
XX CC condition or a susceptibility to a pathological condition in a subject.
XX CC The polynucleotides can also be used to prevent, treat or ameliorate a
XX CC medical condition. The proteins are useful for diagnosis and/or treatment
XX CC of diseases associated with BMPs, in particular bone disorders (e.g.
XX CC osteoarthritis, cartilage defects and tissue repair), and in particular
XX CC for stimulation of angiogenesis. The polynucleotides are useful as
XX CC reagents for differential identification of tissues or cell types present
XX CC in biological samples. The polynucleotides can be used in gene therapy to
XX CC promote the growth of endothelial cells. The present sequence represents
XX CC a BMP of the invention (clone HETAB62)
XX
XX Sequence 345 AA;

```

Query Match

99.6%; Score 1851; DB 3; Length 345;

Best Local Similarity 99.4%; Pred. No. 2,2e-178;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1  MSLEGLLVTSALAGRGTOAESNLSSKQFSSNKKEONGVODPOHERITVSTNGSIHS 60
Db      1  MSLEGLLVTSALAGRGTOAESNLSSKQFSSNKKEONGVODPOHERITVSTNGSIHS 60
QY      61  PRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLDEPEDDICKYDFVEVEEESDGTIL 120
Db      61  PRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLDEPEDDICKYDFVEVEEESDGTIL 120
QY     121  GRMGSGTVPGKOISKGNQIRIRFVSDYFPSEPGFCIHNIYMPQFTEAVSPSVLPSSA 180
Db     121  GRMGSGTVPGKOISKGNQIRIRFVSDYFPSEPGFCIHNIYMPQFTEAVSPSVLPSSA 180
QY     181  LPDLNNATTAFTLEDLIRYLEPERMQLDEDLVYRPTWQLGKAFVFGKRSRVVDNL 240
Db     181  LPDLNNATTAFTLEDLIRYLEPERMQLDEDLVYRPTWQLGKAFVFGKRSRVVDNL 240
QY     241  LTEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLVYKRCGNCACCIANCNBQCVPSPK 300
Db     241  LTEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLVYKRCGNCACCIANCNBQCVPSPK 300
QY     301  VTKKYHEVLQRPKTVGRGLHKSITDVALHHHEBCDCVCRGSTGG 345
Db     301  VTKKYHEVLQRPKTVGRGLHKSITDVALHHHEBCDCVCRGSTGG 345

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Search completed: May 27, 2004, 15:44:44  
Job time : 54 secs

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OM protein - protein search, using sw model

Run on: May 27, 2004, 15:42:51 ; Search time 16.5 Seconds  
(without alignments)  
1079.452 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858  
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Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appli
2	1851	99.6	345	US-09-457-066-2	Sequence 2, Appli
3	1851	99.6	345	US-09-265-686-2	Sequence 2, Appli
4	1851	99.6	345	US-09-540-224-5	Sequence 5, Appli
5	1851	99.6	345	US-09-564-595D-33	Sequence 33, Appli
6	1851	99.6	345	US-09-706-968-2	Sequence 2, Appli
7	1851	99.6	345	US-09-723-749-2	Sequence 2, Appli
8	1851	99.6	345	US-09-823-033-2	Sequence 2, Appli
9	1664	89.6	345	US-09-457-066-43	Sequence 43, Appli
10	1664	89.6	345	US-09-564-595D-35	Sequence 35, Appli
11	1664	89.6	345	US-09-706-968-43	Sequence 43, Appli
12	1664	89.6	345	US-09-823-033-4	Sequence 54, Appli
13	1325	71.3	302	US-09-564-595D-54	Sequence 54, Appli
14	1266.5	68.2	303	US-09-564-595D-57	Sequence 57, Appli
15	1098	59.1	316	US-09-564-595D-55	Sequence 55, Appli
16	1051.5	56.6	317	US-09-564-595D-56	Sequence 56, Appli
17	741.5	39.9	370	US-09-457-066-37	Sequence 37, Appli
18	741.5	39.9	370	US-09-540-224-2	Sequence 2, Appli
19	741.5	39.9	370	US-09-564-595D-2	Sequence 2, Appli
20	741.5	39.9	370	US-09-706-968-37	Sequence 37, Appli
21	741.5	39.9	370	US-09-808-972-2	Sequence 2, Appli
22	741.5	39.9	370	US-09-823-033-5	Sequence 5, Appli
23	737.5	39.7	370	US-09-540-224-4	Sequence 4, Appli
24	737.5	39.7	370	US-09-564-595D-53	Sequence 53, Appli
25	737.5	39.7	370	US-09-808-972-4	Sequence 4, Appli
26	180	9.7	53	US-09-621-976-5212	Sequence 5212, Ap
27	173	9.3	3623	US-09-341-461-2	Sequence 2, Appli

28	172.5	9.3	730	US-08-872-757-2	Sequence 2, Appli
29	172.5	9.3	730	US-09-850-048A-2	Sequence 2, Appli
30	172	9.3	1012	US-09-285-385C-4	Sequence 4, Appli
31	171	9.2	1015	US-09-285-385C-2	Sequence 2, Appli
32	169	9.1	788	US-08-572-225-1	Sequence 1, Appli
33	169	9.1	986	US-09-285-385C-19	Sequence 19, Appli
34	164.5	8.9	909	US-08-936-135-18	Sequence 18, Appli
35	164.5	8.9	909	US-09-439-711C-18	Sequence 18, Appli
36	164.5	8.9	926	US-08-936-135-20	Sequence 20, Appli
37	164.5	8.9	926	US-09-439-711C-20	Sequence 20, Appli
38	164.5	8.9	931	US-09-583-638-4	Sequence 4, Appli
39	163.5	8.8	921	US-09-439-711C-4	Sequence 4, Appli
40	163.5	8.8	922	US-09-116-473-4	Sequence 4, Appli
41	163	8.8	101	US-09-374-135-6	Sequence 6, Appli
42	160.5	8.6	925	US-09-116-473-2	Sequence 2, Appli
43	160.5	8.6	901	US-08-936-135-22	Sequence 22, Appli
44	160.5	8.6	901	US-09-439-711C-22	Sequence 22, Appli
45	160.5	8.6	906	US-08-936-135-24	Sequence 24, Appli

## ALIGNMENTS

RESULT 1  
US-09-040-220D-2  
; Sequence 2, Application US/09040220D  
; Patent No. 6391311  
; GENERAL INFORMATION:  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR  
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC  
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,  
; FILE REFERENCE: P1122  
; CURRENT APPLICATION NUMBER: US/09/040,220D  
; CURRENT FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Human  
US-09-040-220D-2

Query Match	Score	1851;	DB 4;	Length	345;
Beet Local Similarity	99.4%	Pred. No. 6.2e-193;			
Matches	343;	Conervative	2;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	MSFLGLLVTSALAGORRGTQAESNLSSKFOFSKNGVQDPQHERITVSTNGSIHS	60		
Db	1	MSFLGLLVTSALAGORRGTQAESNLSSKFOFSKNGVQDPQHERITVSTNGSIHS	60		
Qy	61	PRFPHYPRNTVLVWLRVAEENWVQLTDERGLEDPEDDICKYDFVEVEPSDGTIL	120		
Db	61	PRFPHYPRNTVLVWLRVAEENWVQLTDERGLEDPEDDICKYDFVEVEPSDGTIL	120		
Qy	121	GRWCGSGTVGKQISKNGQIRIRFVSDEYPPSEGFCHININWPTQTEAVSPVLPPSA	180		
Db	121	GRWCGSGTVGKQISKNGQIRIRFVSDEYPPSEGFCHININWPTQTEAVSPVLPPSA	180		
Qy	121	GRWCGSGTVGKQISKNGQIRIRFVSDEYPPSEGFCHININWPTQTEAVSPVLPPSA	180		
Db	121	GRWCGSGTVGKQISKNGQIRIRFVSDEYPPSEGFCHININWPTQTEAVSPVLPPSA	180		
Qy	181	LPDLNNATITAFSTLBDLIRYLEPBRWQDLBDLYPTQGLKAVFPGKRSVVDNL	240		
Db	181	LPDLNNATITAFSTLBDLIRYLEPBRWQDLBDLYPTQGLKAVFPGKRSVVDNL	240		
Qy	241	LTEFVRLYSCTPRNFVSIREELKRTDTTFWPGCLVRCGNCACCAHNCNEQCVPSK	300		
Db	241	LTEFVRLYSCTPRNFVSIREELKRTDTTFWPGCLVRCGNCACCAHNCNEQCVPSK	300		
Qy	301	VTKKTHEVLDLRPTGVRGLHKSITDVALHHEBCDVCGRSGTG	345		
Db	301	VTKKTHEVLDLRPTGVRGLHKSITDVALHHEBCDVCGRSGTG	345		

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; TYPE: PRT
; ORGANISM: Human

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Qy 181 LPDLLNNNAITAFSTLEDLIRLTPEPERWQOLDEDLYRPTWOLLGKAVFGRGRSVVDNL 240

b 181 LPDLLNNNAITAFSTLEDLIRLTPEPERWQOLDEDLYRPTWOLLGKAVFGRGRSVVDNL 240



QY 241 LTBVRLVYSCPRNFVSIREELKRTDTIIPMGCLVYKCGNACCLHNCNCCQCVPSK 300  
DB 241 LTBVRLVYSCPRNFVSIREELKRTDTIIPMGCLVYKCGNACCLHNCNCCQCVPSK 300  
QY 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHHBECDCVCRSGTG 345  
DB 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHHBECDCVCRSGTG 345

## RESULT 5

US-09-564-595D-33  
Sequence 33, Application US/09564595D  
Patent No. 6495668  
GENERAL INFORMATION:  
APPLICANT: Gilbert, Teresa  
APPLICANT: Hart, Charles E.  
APPLICANT: Sheppard, Paul O.  
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
FILE REFERENCE: 99-19  
CURRENT APPLICATION NUMBER: US/09/564,595D  
CURRENT FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: US 09/304,216  
PRIOR FILING DATE: 1999-05-03  
PRIOR APPLICATION NUMBER: US 60/164,463  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: US 60/180,169  
PRIOR FILING DATE: 2000-02-04  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-564-595D-33

Query Match 99.6%; Score 1851; DB 4; Length 345;  
Best Local Similarity 99.4%; Pred. No. 6.2e-193;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTLSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
DB 1 MSFLGLLVTLSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
QY 61 PRPHTYPRNTVLVWRLVAEENWVQLTFDERGLDEPDDICKYDFVEVEBPDGTL 120  
DB 61 PRPHTYPRNTVLVWRLVAEENWVQLTFDERGLDEPDDICKYDFVEVEBPDGTL 120  
QY 121 GRWCGSTVPGKQISKNQIRIRFVSDYFSEBPGFCIHNIWMPQTEAVSPSLPPSA 180  
DB 121 GRWCGSTVPGKQISKNQIRIRFVSDYFSEBPGFCIHNIWMPQTEAVSPSLPPSA 180  
QY 181 LPDLNNATTAFTSTLEDLIRYLEBERWQDLEDLYRPTWQLGKAVFGKRSRVVDNL 240  
DB 181 LPDLNNATTAFTSTLEDLIRYLEBERWQDLEDLYRPTWQLGKAVFGKRSRVVDNL 240  
QY 241 LTBVRLVYSCPRNFVSIREELKRTDTIIPMGCLVYKCGNACCLHNCNCCQCVPSK 300  
DB 241 LTBVRLVYSCPRNFVSIREELKRTDTIIPMGCLVYKCGNACCLHNCNCCQCVPSK 300  
QY 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHHBECDCVCRSGTG 345  
DB 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHHBECDCVCRSGTG 345

## RESULT 6

US-09-706-968-2  
Sequence 2, Application US/09706968  
Patent No. 6528050  
GENERAL INFORMATION:  
APPLICANT: Gao, Zeren  
APPLICANT: Hart, Charles E.  
APPLICANT: Piddington, Christopher S.  
APPLICANT: Sheppard, Paul O.

APPLICANT: Shoemaker, Kimberly E.  
APPLICANT: Gilbertson, Debra G.  
APPLICANT: West, James W.  
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
FILE REFERENCE: 98-60C1  
CURRENT APPLICATION NUMBER: US/09/706,968  
CURRENT FILING DATE: 2000-11-06  
PRIOR APPLICATION NUMBER: US/09/541,752  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-706-968-2

Query Match 99.6%; Score 1851; DB 4; Length 345;  
Best Local Similarity 99.4%; Pred. No. 6.2e-193;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTLSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
DB 1 MSFLGLLVTLSALAGORGTQAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
QY 61 PRPHTYPRNTVLVWRLVAEENWVQLTFDERGLDEPDDICKYDFVEVEBPDGTL 120  
DB 61 PRPHTYPRNTVLVWRLVAEENWVQLTFDERGLDEPDDICKYDFVEVEBPDGTL 120  
QY 121 GRWCGSTVPGKQISKNQIRIRFVSDYFSEBPGFCIHNIWMPQTEAVSPSLPPSA 180  
DB 121 GRWCGSTVPGKQISKNQIRIRFVSDYFSEBPGFCIHNIWMPQTEAVSPSLPPSA 180  
QY 181 LPDLNNATTAFTSTLEDLIRYLEBERWQDLEDLYRPTWQLGKAVFGKRSRVVDNL 240  
DB 181 LPDLNNATTAFTSTLEDLIRYLEBERWQDLEDLYRPTWQLGKAVFGKRSRVVDNL 240  
QY 241 LTBVRLVYSCPRNFVSIREELKRTDTIIPMGCLVYKCGNACCLHNCNCCQCVPSK 300  
DB 241 LTBVRLVYSCPRNFVSIREELKRTDTIIPMGCLVYKCGNACCLHNCNCCQCVPSK 300  
QY 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHHBECDCVCRSGTG 345  
DB 301 VTKKYHEVLQLRPKTVGVLGKSLTDVALBHHBECDCVCRSGTG 345

## RESULT 7

US-09-723-749-2  
Sequence 2, Application US/09723749  
Patent No. 6620784  
GENERAL INFORMATION:  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Kuo, Sophia S.  
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
FILE REFERENCE: P1122B2D1  
CURRENT APPLICATION NUMBER: US/09/723,749  
CURRENT FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: US 09/265,686  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: US 09/040,220  
PRIOR FILING DATE: 1998-03-17  
PRIOR APPLICATION NUMBER: US 09/184,216  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 8  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Human  
US-09-723-749-2

Query Match 99.6%; Score 1851; DB 4; Length 345;  
Best Local Similarity 99.4%; Pred. No. 6.2e-193;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLLVTSALAGORGTQAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60  
 DB 1 MSIFGLLLVTSALAGORGTQAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60  
 QY 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDDICTKYPVEEPPSDGTTIL 120  
 DB 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDDICTKYPVEEPPSDGTTIL 120  
 QY 121 GRWGSSTVPGKQISKGNQIRIRFVSDEYFSPSGFCIHNIYMPQTEAVSPVLPPSA 180  
 DB 121 GRWGSSTVPGKQISKGNQIRIRFVSDEYFSPSGFCIHNIYMPQTEAVSPVLPPSA 180  
 QY 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLIEDLYRPTWQLLGKAFVFGKSRVVDNL 240  
 DB 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLIEDLYRPTWQLLGKAFVFGKSRVVDNL 240  
 QY 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
 DB 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
 QY 301 VTKKYHEVLQLRPKTGVRLHKSJLTDVLEHHEBCDVCRCGSTGG 345  
 DB 301 VTKKYHEVLQLRPKTGVRLHKSJLTDVLEHHEBCDVCRCGSTGG 345

RESULT 8  
 US-09-823-033-2  
 ; Sequence 2, Application US/09823033  
 ; Patent No. 663870  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hart, Charles E.  
 ; APPLICANT: Gilbertson, Debra G.  
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
 ; FILE REFERENCE: 00-12  
 ; CURRENT APPLICATION NUMBER: US/09/823,033  
 ; CURRENT FILING DATE: 2001-03-29  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 345  
 ; TYPE: PRN  
 ; ORGANISM: Homo sapiens  
 US-09-823-033-2

Query Match 99.6%; Score 1851; DB 4; Length 345;  
 Best Local Similarity 99.4%; Pred. No. 6.2e-193;  
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLLVTSALAGORGTQAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60  
 DB 1 MSIFGLLLVTSALAGORGTQAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60  
 QY 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDDICTKYPVEEPPSDGTTIL 120  
 DB 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDDICTKYPVEEPPSDGTTIL 120  
 QY 121 GRWGSSTVPGKQISKGNQIRIRFVSDEYFSPSGFCIHNIYMPQTEAVSPVLPPSA 180  
 DB 121 GRWGSSTVPGKQISKGNQIRIRFVSDEYFSPSGFCIHNIYMPQTEAVSPVLPPSA 180  
 QY 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLIEDLYRPTWQLLGKAFVFGKSRVVDNL 240  
 DB 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLIEDLYRPTWQLLGKAFVFGKSRVVDNL 240  
 QY 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
 DB 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
 QY 301 VTKKYHEVLQLRPKTGVRLHKSJLTDVLEHHEBCDVCRCGSTGG 345  
 DB 301 VTKKYHEVLQLRPKTGVRLHKSJLTDVLEHHEBCDVCRCGSTGG 345

RESULT 9  
 US-09-457-066-43  
 ; Sequence 43, Application US/09457066  
 ; Patent No. 6432673  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gao, Zeren  
 ; APPLICANT: Hart, Charles E.  
 ; APPLICANT: Piddington, Christopher S.  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Shoemaker, Kimberly E.  
 ; APPLICANT: Gilbertson, Debra G.  
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
 ; FILE REFERENCE: 98-60  
 ; CURRENT APPLICATION NUMBER: US/09/457,066  
 ; CURRENT FILING DATE: 1999-12-07  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 43  
 ; LENGTH: 345  
 ; TYPE: PRN  
 ; ORGANISM: Mus musculus  
 US-09-457-066-43

Query Match 89.6%; Score 1664; DB 4; Length 345;  
 Best Local Similarity 86.7%; Pred. No. 1.4e-172;  
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSIFGLLLVTSALAGORGTQAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60  
 DB 1 MSIFGLLLVTSALAGORGTQAESNLSSKFQSSNKQNGVODPOHERIITVSTNGSIHS 60  
 QY 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDDICTKYPVEEPPSDGTTIL 120  
 DB 61 PRPHYTPRNTVLMWRLVAEENWMIQITPDERFGLDEPDDICTKYPVEEPPSDGTTIL 120  
 QY 121 GRWGSSTVPGKQISKGNQIRIRFVSDEYFSPSGFCIHNIYMPQTEAVSPVLPPSA 180  
 DB 121 GRWGSSTVPGKQISKGNQIRIRFVSDEYFSPSGFCIHNIYMPQTEAVSPVLPPSA 180  
 QY 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLIEDLYRPTWQLLGKAFVFGKSRVVDNL 240  
 DB 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLIEDLYRPTWQLLGKAFVFGKSRVVDNL 240  
 QY 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
 DB 241 LTBEEVRLYSTCPNPFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
 QY 301 VTKKYHEVLQLRPKTGVRLHKSJLTDVLEHHEBCDVCRCGSTGG 345  
 DB 301 VTKKYHEVLQLRPKTGVRLHKSJLTDVLEHHEBCDVCRCGSTGG 345

RESULT 10  
 US-09-564-595D-35  
 ; Sequence 35, Application US/09564595D  
 ; Patent No. 643668  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilbert, Teresa  
 ; APPLICANT: Hart, Charles E.  
 ; APPLICANT: Sheppard, Paul O.  
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
 ; FILE REFERENCE: 99-19  
 ; CURRENT APPLICATION NUMBER: US/09/564,595D  
 ; CURRENT FILING DATE: 2000-05-03  
 ; PRIOR APPLICATION NUMBER: US 09/304,216  
 ; PRIOR FILING DATE: 1999-05-03  
 ; PRIOR APPLICATION NUMBER: US 60/164,463  
 ; PRIOR FILING DATE: 1999-11-10  
 ; PRIOR APPLICATION NUMBER: US 60/180,169  
 ; PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57  
 SOFTWARE: PaetsEQ for Windows Version 4.0  
 SEQ ID NO 35  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-564-595D-35

Query Match 89.6%; Score 1664; DB 4; Length 345;  
 Best Local Similarity 86.7%; Pred. No. 1.4e-172;  
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSSKFOSSNKEONGVODPOHERIITVSTNGSIHS 60  
 DB 1 MLUGLLLTLSALAGRGTRAESNLSSKLOSSDKXONGVODPRHERVVTISNGSIHS 60  
 QY 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDICKYDFVEVEBPSDGTIL 120  
 DB 61 PKPHTYPRNVLVWRLVAEENWVIOITFDERFGLDEPDICKYDFVEVEBPSDGSVL 120  
 QY 121 GRMGSGTVPGKQSKGNQIRIRFVSDEYFSEBPGFCHINIVMPQTEAVSPSVLPSSA 180  
 DB 121 GRMGSGTVPGKQSKGNHIRIRFVSDEYFSEBPGFCHISIIIMPQTEITSPSVLPSS 180  
 QY 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLDELYPTWOLGKAFVGRKSRVNDL 240  
 DB 181 LSLDLINNAITAFSTLEDLIRYLEBDRWQDLDSLYKTWOLGKAFVGRKSKVNDL 240  
 QY 241 LTBEEVLYSCTPRNFSVSIREELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCVPSK 300  
 DB 241 LKEEVLYSCTPRNFSVSIREELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCVPRK 300  
 QY 301 VTKKYHEVLQLRPTKTVGGLHKSITDVALBHEHEBCDCVCRSTGG 345  
 DB 301 VTKKYHEVLQLRPTKTVGGLHKSITDVALBHEHEBCDCVCRNAGG 345

RESULT 11  
 US-09-706-968-43  
 Sequence 43, Application US/09706968  
 Patent No. 6528050  
 GENERAL INFORMATION:  
 APPLICANT: Gao, Zeren  
 APPLICANT: Hart, Charles E.  
 APPLICANT: Piddington, Christopher S.  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Shoemaker, Kimberly E.  
 APPLICANT: Gilbertson, Debra G.  
 TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGFS  
 FILE REFERENCE: 98-60C1  
 CURRENT APPLICATION NUMBER: US/09/706, 968  
 CURRENT FILING DATE: 2000-11-06  
 PRIOR APPLICATION NUMBER: US/09/541, 752  
 PRIOR FILING DATE: 2000-03-31  
 NUMBER OF SEQ ID NOS: 50  
 SOFTWARE: PaetsEQ for Windows Version 3.0  
 SEQ ID NO 43  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-706-968-43

Query Match 89.6%; Score 1664; DB 4; Length 345;  
 Best Local Similarity 86.7%; Pred. No. 1.4e-172;  
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSSKFOSSNKEONGVODPOHERIITVSTNGSIHS 60  
 DB 1 MLUGLLLTLSALAGRGTRAESNLSSKLOSSDKXONGVODPRHERVVTISNGSIHS 60  
 QY 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDICKYDFVEVEBPSDGTIL 120  
 DB 61 PKPHTYPRNVLVWRLVAEENWVIOITFDERFGLDEPDICKYDFVEVEBPSDGSVL 120

DB 61 PKPHTYPRNVLVWRLVAEENWVIOITFDERFGLDEPDICKYDFVEVEBPSDGSVL 120  
 QY 121 GRMGSGTVPGKQSKGNQIRIRFVSDEYFSEBPGFCHINIVMPQTEAVSPSVLPSSA 180  
 DB 121 GRMGSGTVPGKQSKGNHIRIRFVSDEYFSEBPGFCHISIIIMPQTEITSPSVLPSS 180  
 QY 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLDELYPTWOLGKAFVGRKSRVNDL 240  
 DB 181 LSLDLINNAITAFSTLEDLIRYLEBDRWQDLDSLYKTWOLGKAFVGRKSKVNDL 240  
 QY 241 LTBEEVLYSCTPRNFSVSIREELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCVPSK 300  
 DB 241 LKEEVLYSCTPRNFSVSIREELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCVPRK 300  
 QY 301 VTKKYHEVLQLRPTKTVGGLHKSITDVALBHEHEBCDCVCRSTGG 345  
 DB 301 VTKKYHEVLQLRPTKTVGGLHKSITDVALBHEHEBCDCVCRNAGG 345

RESULT 12  
 US-09-823-033-4  
 Sequence 4, Application US/09823033  
 Patent No. 6663870  
 GENERAL INFORMATION:  
 APPLICANT: Hart, Charles E.  
 APPLICANT: Gilbertson, Debra G.  
 TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
 FILE REFERENCE: 00-12  
 CURRENT APPLICATION NUMBER: US/09/823, 033  
 CURRENT FILING DATE: 2001-03-29  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PaetsEQ for Windows Version 3.0  
 SEQ ID NO 4  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-823-033-4

Query Match 89.6%; Score 1664; DB 4; Length 345;  
 Best Local Similarity 86.7%; Pred. No. 1.4e-172;  
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGRGTOAESNLSSKFOSSNKEONGVODPOHERIITVSTNGSIHS 60  
 DB 1 MLUGLLLTLSALAGRGTRAESNLSSKLOSSDKXONGVODPRHERVVTISNGSIHS 60  
 QY 61 PRPHYPRNTVLVWRLVAEENWVIOITFDERFGLDEPDICKYDFVEVEBPSDGTIL 120  
 DB 61 PKPHTYPRNVLVWRLVAEENWVIOITFDERFGLDEPDICKYDFVEVEBPSDGSVL 120  
 QY 121 GRMGSGTVPGKQSKGNQIRIRFVSDEYFSEBPGFCHINIVMPQTEAVSPSVLPSSA 180  
 DB 121 GRMGSGTVPGKQSKGNHIRIRFVSDEYFSEBPGFCHISIIIMPQTEITSPSVLPSS 180  
 QY 181 LPDLINNAITAFSTLEDLIRYLEPERWQDLDELYPTWOLGKAFVGRKSRVNDL 240  
 DB 181 LSLDLINNAITAFSTLEDLIRYLEBDRWQDLDSLYKTWOLGKAFVGRKSKVNDL 240  
 QY 241 LTBEEVLYSCTPRNFSVSIREELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCVPSK 300  
 DB 241 LKEEVLYSCTPRNFSVSIREELKRTDTIIFWPGCLVYKRCGNCACCLHNCNCCVPRK 300  
 QY 301 VTKKYHEVLQLRPTKTVGGLHKSITDVALBHEHEBCDCVCRSTGG 345  
 DB 301 VTKKYHEVLQLRPTKTVGGLHKSITDVALBHEHEBCDCVCRNAGG 345

RESULT 13  
 US-09-564-595D-54  
 Sequence 54, Application US/09564595D  
 Patent No. 6495668  
 GENERAL INFORMATION:



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Db      121  QFTAEATWESVTSSISGVSYNSPSPVTDPT-LIADALDKXIAEFDVEDLKYFNPEBMO 179
QY      210  LDLEDLYRPTWQJGKAFFGKSRVNDLNLTEBVLXCTPRNFSYSIREELKRTDTI 269
Db      180  EDLENMYLDTPRYGRGRY-HDRKSK-VDLRLINDDAKRYSCTPRNVSYNIREELKANV 237
QY      270  FMPGCLLVKRCGNACCLHNCNECQCVPSKVTKKYHEVLOLRP---KTGVRGLHKS/LTD 326
Db      238  FPRCLVYQRCGNGCCTVWNRSTCNSGKTVKKYHEVLOPFBGHIKRGRAKTMALVD 297
QY      327  VALHHEECDCVC 339
Db      298  IQLDHHERCDCIC 310

```

Search completed: May 27, 2004, 15:48:08  
 Job time : 17.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:41:56 ; Search time 14 Seconds  
(without alignments)  
2370.434 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858  
Sequence: 1 MSLEGLLVTSALAGQRGRG.....DVALEHHECDCCVCRGRTG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	742.5	40.0	370	2	UC7591
2	737.5	39.7	370	2	UC7598
3	736	39.6	370	2	UC7592
4	183	9.8	3623	2	TC9456
5	181.5	9.8	730	1	BMH1
6	179.5	9.7	927	1	UC0948
7	176	9.5	707	2	UC2218
8	176	9.5	3623	2	TC9456
9	173	9.3	823	1	AS8788
10	169	9.1	991	2	UC9540
11	169	9.1	991	2	UC9540
12	154	8.3	449	2	UC5362
13	148.5	8.0	1057	1	UC9288
14	143.5	7.7	686	1	UC9271
15	139.5	7.5	1070	2	UC71069
16	138.5	7.5	597	2	UC71352
17	138	7.4	705	1	UC10018
18	137.5	7.4	699	1	UC10018
19	137.5	7.4	1524	2	UC10018
20	135	7.3	533	2	UC7985
21	133	7.2	1594	2	UC10549
22	132	7.1	419	2	UC69207
23	130.5	7.0	1464	2	UC69207
24	128	6.9	402	2	UC69207
25	127.5	6.9	757	2	UC69207
26	127.5	6.9	3871	2	UC69207
27	125	6.7	198	2	UC69207
28	123.5	6.6	277	2	UC69207
29	123.5	6.6	579	2	UC69207

30	120.5	6.5	245	1	UC7591	platelet-derived g
31	120.5	6.5	275	2	UC6506	tumor necrosis fac
32	118.5	6.4	276	2	UC7290	TSG-6 homolog p54
33	114.5	6.2	148	2	UC9530	16k vascular endot
34	114.5	6.2	241	1	UC9530	platelet-derived g
35	112.5	6.1	200	2	UC9530	platelet-derived g
36	112.5	6.1	215	2	UC9530	platelet-derived g
37	112.5	6.1	226	2	UC9530	platelet-derived g
38	111.5	6.0	319	2	UC9530	platelet-derived g
39	110.5	5.9	2403	2	UC9530	platelet-derived g
40	110	5.9	166	2	UC9530	platelet-derived g
41	109	5.9	197	2	UC9530	platelet-derived g
42	108.5	5.8	126	1	UC9530	platelet-derived g
43	108	5.8	196	2	UC9530	platelet-derived g
44	104.5	5.6	232	2	UC9530	platelet-derived g
45	104	5.6	196	2	UC9530	platelet-derived g

## ALIGNMENTS

RESULT 1									
UC7591									
spinal cord-derived growth factor-B precursor - human									
C:Species: Homo sapiens (man)									
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001									
C:Accession: UC7591									
R:Hamada, T.; Ue-Tai, K.; Imaki, J.; Miyata, Y.									
Biochem. Biophys. Res. Commun. 280, 733-737, 2001									
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C									
A:Reference number: UC7591; PMID:21092670; PMID:11162582									
A:Accession: UC7591									
A:Molecule type: DNA									
A:Residues: 1-370 <HAM>									
A:Cross-references: DDBJ:AB033832									
C:Genetics:									
A:Gene: scdgb-B									
F:1-17/Domain: secretory signal sequence #status predicted <SIG>									
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>									
F:152-170/Region: CUB domain #status predicted									
F:1272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gro									
F:1294-308/Region: conserved motif #status predicted									
Query Match									
Best Similarity 40.0%; Score 742.5; DB 2; Length 370;									
Best Local Similarity 43.6%; Pred. No. 9e-57;									
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;									
QY	3	LEGLLVTSALAGQRGRGTAESNLTKQFSSN--KEONGVOD-POHERITVSTNGSI	58						
DB	5	IFVYTLICANFCSCGRDTSATFQASIKALRNANLRDSENLTLDRDETIVKNGYV	64						
QY	59	HSPPPHPTYPNTLVLRVAEENWMIQLTDFERFGLDEDDICRYFVEVEPSDGT	118						
DB	65	QSPFPNPSYPNLLITLRLHS-QENTRIQLVFDNQFGLAEANDICRYFVEVEDISRTS	123						
QY	119	--IIGRWGSGCTVCGKQISKNOIRIRFVSPSEVPSRPGCIHINIMVQPTAV----	171						
DB	124	TIIRGWRGKHKEVPRIKSRNQIKITKPSDSDYVAAGFITYLSL-LEDRQPAASSTN	182						
QY	172	-----SPGLPSPALPLDLNNAITAFSTLEDLIRYLEPERQDLLELYR	217						
DB	183	WESYTSISGVSVNPSVTDPT-LIADALDKKIAEFPTVEDLLKFPNDSQEDLENNYL	241						
QY	218	PTWOLGKAIFYGKRSKRVVDNLITTEVRYSCTPRNPSVIRELKTDTTIPMGCLLV	277						
DB	242	DTPRYGRSY-HSRKSK-VLDRLINDAKYSCPRNYSVIRELKLAVNVPFPCLLV	299						
QY	278	KRCGNGACCLANNGECQVPSKYTKYHYVQLQRP---KTVGGLKSLTDVLAHHEE	334						
DB	300	QRCGNGCGCTVNRSCNCSGKTVKTYHEVLPBPGHTRGRGAKTMALVDLDHHR	359						
QY	335	CDVC 339							

Db 360 CDCIC 364

## RESULT 2

JC7998 platelet-derived growth factor-D - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Nov-2003 #sequence\_revision 10-Nov-2003 #text\_change 24-Nov-2003

C/Accession: JC7998

R/Zhuo, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Laeky, J.A.

Biochem. Biophys. Res. Commun. 308, 126-132, 2003

A/Title: A novel murine PDGF-D splicing variant results in significant differences in p

A/Reference number: JC7998; PMID:12890490

A/Accession: JC7998

A/Molecule type: mRNA

A/Residues: 1-370 &lt;ZHU&gt;

C/Comment: This protein is a potent mesenchymal cell mitogen and chemottractant involve

C/Genetics:

A/Gene: pdgfr-d

A/Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2

C/Keywords: fibrosis; PDGF-D

## Query Match

Best Local Similarity 39.7%; Score 737.5; DB 2; Length 370;

Matches 153; Conservative 59; Mismatches 103; Indels 33; Gaps 9;

Db 16 QRRGTOAESNLSSKFOFSSNKEQNGVOD-PQHERITVSTNGSIHSPRPHTYPRNTLV 74

26 QRRASIRAKRANR-----RDESNHLDLYORENIGVTSNGHVQSPRFPNSIPRNLILT 80

Db 75 WRLVAEENWVIOUPTDERFGLDEPDDEICKYDFVEVEBPSDGT--ILGRWCGSGTVPGK 132

81 WMLRS-OEKTRIDLSFHQFGLAEANDICRYDFVEVEBPSDGT--ILGRWCGSGTVPGK 139

Db 133 QISKGNQIRIRFVSDEPSEBPCIHYNVMPQFTAV-----SPS 174

140 ITRTQIKITTFKSDDFVAKPGKITYSFVEDPQPAASSETWSESTVVRGWHGCKHEIPR 199

Db 175 VLPSPALPLDNLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSR 234

200 ITDPT-LTDALDKTVAEPFTVEDLKHFPVSMQDLELYDTPIYRGRSY-HDRKSK 257

Db 235 VVDNLITTEVRLYSCTPNPFVSIREELKRTDTITPFGCLYKRCGNCACCLHNCNC 294

258 -VDLDRLNDLVKYSCTPRNHSVLRBELKLITNAVFPRCLIVQRCGNGCGCTVWVWKC 316

Db 295 QCVPSKYTKYKHEVLOLRP---KTGVRGLHKSILTDVALHNEBCDVC 339

317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Db 317 TCSSGKTVKRYKHEVLFKPEGRFKRGRKAKMALVDIQLDHERKDCIC 364

Query Match 39.6%; Score 736; DB 2; Length 370;  
 Best Local Similarity 45.6%; Pred. No. 3.3e-56;  
 Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;

Db 37 EQNGVOD-PQHERITVSTNGSIHSPRPHTYPRNTLVWRLVAEENWVIOUPTDERRG 95

42 ESNHLDLYRDRDNINVTGTHVQSPRFPNSYRNLITWRLMS-OEKTRIDLAIPHQFG 100

Db 96 LEDPEDDICKYDFVEVEBPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEPSE 153

101 LBEAENDICKYDFVEVEBPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEPSE 160

Db 154 PGFCIHYNIV--MPOFTAV-----SPSVLPSPALPLDNLNNAITAFST 195

161 PGKITYSFVEDPQPAASSETWSESTVVRGWHGCKHEIPRITSRKQIKITFQSDDFVAK 219

Db 196 LEDLITTEVRLYSCTPNPFVSIREELKRTDTITPFGCLYKRCGNCACCLHNCNC 255

220 VEDLITTEVRLYSCTPNPFVSIREELKRTDTITPFGCLYKRCGNCACCLHNCNC 277

Db 256 SVSIREELKRTDTITPFGCLYKRCGNCACCLHNCNCQCVPSKYTKYKHEVLOLRP-- 313

278 SVNLREELKLITNAVFPRCLIVQRCGNGCGCTVWVWKCCTSSGKTVKRYKHEVLFKPEGR 337

Db 314 -KTGVRGLHKSILTDVALHNEBCDVC 339

338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364

Db 338 FKRGRKAKMALVDIQLDHERKDCIC 364



QY 237 DLNLTFR--EVR-----LY--SCTPRNFSVSIREBK-RDPTI-----FM 271  
 DB 1100 G-NYTFLELRIDGGEYKSPLLGIFYSGNLPPTIISHNKLMLKFSQIDTRSGFSAYW 1158  
 QY 272 PGCLLVKRCGNGACACCHNCNECQVPSKVTKKYHE---VLQLRPKGVRLHSLRDVA 328  
 DB 1159 DGS--STGCCGN-----LTTSGGTISRNYPMYPYHSHSECTYWLKSSHC-SAFELERFDHF 1211  
 QY 329 LEHHEEC 335  
 DB 1212 LEHHPNC 1218  
 RESULT 5  
 BMH01  
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human  
 N/Alternate names: bone morphogenic protein 1 (BMP1)  
 C/Species: Homo sapiens (man)  
 C/Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999  
 C/Accession: A37278; E58788  
 R/Mozney, J.M.; Rosen, V.; Celaste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew  
 A/Title: Novel regulators of bone formation: molecular clones and activities.  
 A/Reference number: A37278; MUID:89072730; PMID:3201241  
 A/Accession: A37278  
 A/Molecule type: mRNA  
 A/Residues: 1-730 <WQ2>  
 A/Cross-references: GB:M2488; NID:G179499; PIDN:AAA51833.1; PID:G179500  
 C/Genetics:  
 A/Gene: GDB:BMP1  
 A/Cross-references: GDB:125203; OMIM:112264  
 A/Map position: 8p21-8p21  
 C/Function:  
 A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type  
 C/Superfamily: procollagen C-endopeptidase; asparagin homology; Ctr/Cis repeat homology; E  
 C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl  
 F:1-22/Domain: signal sequence #status predicted <sig>  
 F:23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>  
 F:130-321/Domain: asparagin homology <Asp>  
 F:332-431/Domain: Ctr/Cis repeat homology <CTR2>  
 F:435-544/Domain: Ctr/Cis repeat homology <CTR2>  
 F:551-587/Domain: EGF homology <EGF>  
 F:551-700/Domain: Ctr/Cis repeat homology <CTR3>  
 F:91,142,332,363,599/Binding site: carbonylcarboxylate (Asn) (covalent) #status predicted  
 F:153-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66  
 F:213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted  
 F:214/Active site: Glu #status predicted  
 F:555/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 Query Match 9.8%; Score 181.5; DB 1; Length 730;  
 Best Local Similarity 37.3%; Pred. No. 1.4e-07;  
 Matches 50; Conservative 20; Mismatches 47; Indels 17; Gaps 7;  
 QY 55 NGSHSRPHTYRNTVLVRLVA-VEENWIDLTDERGLEDPPDDICKYPVEVE 113  
 DB 599 NGSTTSQWPKPEYPPNKKMQLVAFQYRISLQDFDFETEG-----NDVCKYDFEVR 653  
 QY 114 --PSDGTILGRMGSGTVPEKQISKGNQIRIRFVSDEVPSPGCTHYNTVMQFTEAV 171  
 DB 654 GLTADSLKHKFGCS -EKPEVITISQYNNMVRFEKSDMTV-SKKGFKAHF-----PSK- 704  
 QY 172 SPVSVPSPALPLDL 185  
 DB 705 RPAQOPRGRPHQL 718  
 RESULT 6  
 JQ0948  
 A5 antigen precursor - African clawed frog  
 C/Species: Xenopus laevis (African clawed frog)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
 C/Accession: JH0466; JQ0948

R/Takagi, S.; Hirata, T.; Agata, K.; Mochi, M.; Eguchi, G.; Fujisawa, H.  
 Neuron 7, 295-307, 1991  
 A/Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homolog  
 A/Reference number: JH0466; MUID:91337458; PMID:1908252  
 A/Accession: JH0466  
 A/Molecule type: mRNA  
 A/Residues: 1-927 <TK>  
 A/Cross-references: GB:D10467; GB:D01077; NID:q222962; PIDN:BA01260.1; PID:q222963  
 A/Experimental source: tadpole, brain  
 A/Note: This protein has motifs homologous to complement components Ctr and Cts and to  
 C/Comment: This protein is a neuronal cell surface molecule involved in the neuronal re  
 C/Superfamily: Xenopus A5 antigen; Ctr/Cis repeat homology; discoidin I amino-terminal  
 C/Keywords: duplication; glycoprotein; transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <sig>  
 F:22-927/Product: A5 antigen #status predicted <Asp>  
 F:27-138/Domain: Ctr/Cis repeat homology <CTR1>  
 F:147-262/Domain: Ctr/Cis repeat homology <CTR2>  
 F:274-424/Domain: discoidin I amino-terminal homology <DN1>  
 F:430-584/Domain: discoidin I amino-terminal homology <DN2>  
 F:646-812/Domain: MAM homology <MAM>  
 F:861-883/Domain: transmembrane #status predicted <TM>  
 F:150,261,300,523,844/Binding site: carbonylcarboxylate (Asn) (covalent) #status predicted  
 Query Match 9.7%; Score 179.5; DB 1; Length 927;  
 Best Local Similarity 31.6%; Pred. No. 2.9e-07;  
 Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;  
 QY 50 ITVSTNGSIHSPRPHRYNTVLVRLVAEENWIDLTDERGLEDPPDDICKYPV 109  
 DB 31 IKITSPEYLSAGVPHSYPPSPORCEMLIQAPBEHQRIIMINPNHFDLEDE--CKYDYV 87  
 QY 110 EV--EESDGTILGRMGSGTVPEKQISKGNQIRIRFVSDEVPSPGCTHYNTVM 165  
 DB 88 EVIDGDMAQQLGKCYGK-IAPSPVSTSPSIFIRFVSDEYETPG-AGFSIRREVFKTPG 145  
 QY 166 ----QPTFA--VSPSVLPSPALPLDLNNAITVASTLEDIRYDEPRMOLD 213  
 DB 146 EGSNFTSNQVSKPKYPRKRYALCECTYITRAPKQETV--LEFSFLEAD 197  
 RESULT 7  
 JQ2218  
 procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)  
 N/Alternate names: bone morphogenic protein 1  
 C/Species: Xenopus laevis (African clawed frog)  
 C/Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Sep-1999  
 C/Accession: JQ2218  
 R/Memo, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Xung, H.  
 Gene 134, 257-261, 1993  
 A/Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prot  
 A/Reference number: JQ2218; MUID:94085787; PMID:8262384  
 A/Accession: JQ2218  
 A/Molecule type: mRNA  
 A/Residues: 1-707 <MA>  
 A/Cross-references: GB:112249; NID:q406540; PIDN:AA15313.1; PID:q406541  
 C/Comment: This protein induces ectopic cartilage formation in vivo.  
 C/Superfamily: procollagen C-endopeptidase; asparagin homology; Ctr/Cis repeat homology;  
 C/Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc  
 F:93-284/Domain: asparagin homology <Asp>  
 F:93-397/Region: complement 1r/1s-like repeat  
 F:285-394/Domain: Ctr/Cis repeat homology <CTR1>  
 F:358-510/Region: complement 1r/1s-like repeat  
 F:358-507/Domain: Ctr/Cis repeat homology <CTR2>  
 F:514-550/Domain: EGF homology <EGF>  
 F:554-666/Region: complement 1r/1s-like repeat  
 F:554-663/Domain: Ctr/Cis repeat homology <CTR3>  
 F:62,105,295,326/Binding site: carbonylcarboxylate (Asn) (covalent) #status predicted  
 F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F:177/Active site: Glu #status predicted  
 F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 Query Match 9.5%; Score 176; DB 2; Length 707;  
 Best Local Similarity 43.3%; Pred. No. 4.2e-07;

	Matches	45;	Conservative	15;	Mismatches	36;	Indels	8;	Gaps	5;
Qy	55	NGSIHSPRPHTY	PENTLWRLVA	VEENVWV	QLTFEDRFG	LEDEDDI	CKYDF	VEYEB-	113	
Db	562	NGSINSPGMPKEX	PPNNKNCIMQ	VLAPTC	YRSLKFDQ---	PETSGNDV	CKTDF	VEYV	ASG	617
Qy	114	-PSDGTILGRWC	GSGTVPEKQ	ISKGNQIR	IRPVSDEY	PPSPDEGF	156			
Db	618	LTSQSLKHGKFGS-	ELPAVITTSQ	NNMKITEKSN	NTV-SKKG	GF	659			

```

RESULT 8
T08618
Intrinsic factor-B12 receptor CUBILIN precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence
C:Revision: 11-Jun-1999 #text_change 02-Aug-2002
C:Accession: T08618
R:Mostrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kayser, J.H.; Rasmussen, H.H.; Braut,
J. Biol. Chem. 273, 5235-5242, 1998
A:Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A:Reference number: Z16459; MUID:98148073; PMID:9478979
A:Accession: T08618
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3623 <MOE>
A:Cross-references: EMBL:AF022247; NID:G3834379; PIDN:AAC71661.1; PID:G3834380
C:Genetics:
A:Gene: CUBILIN
C:Superfamily: Intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F:1-20/Domain: signal sequence #status predicted <Sig>
F:21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <Mat>
F:13-164/Domain: EGF homology <EGF>
F:436-467/Domain: EGF homology <EGF>

```

Query Match	9.5%;	Score	176;	DB 2;	Length	3623;	
Best Local Similarity	25.5%;	Score	No.3.3e-06;				
Matches	95;	Mismatches	133;	Indels	92;	Gaps	24;

QY	2	SLPGLLVT--SALAGORGRQAESNLSSKQFSSCNKONGQVDPQHRRIITVSNQSIH	59
Dh	901	SVNIILYTFYKSSSMENRGTFA-----KSSDKIECG-----EVLTAI--GLIE	944
QY	60	SPRPHTYPRNTVLWRLVAVEENWIQLTFDERGLEDPEDDICKYQFVEVEEPPSDGTI	119
Dh	945	SPGHNNYPRGNNCTWYHV-VQROGLILNTESS-FYLEFHN--CTNDYLETYDAATF	1000
QY	120	LGRMGSGSTVPEKQIKSKNQIRIRFVSDEYPPSEPGFCIHY-----NIWMPQTEAVSP	173
Dh	1001	LGRYCGK-SIPPSILTSNSIKLIFVSSALAHG-GFISINVEALDASSVCYDYDNDNGM	1058
QY	174	SVLP--PEALPDL-----LNNAL-----TAFSTLED-----LNIYLEBERNQDLE	213
Dh	1059	LSSPRFFPNNYSNNECIYRIYVGLNQQLALHPTDF-TLEDYFGSOCDVFE-----IR	1110
QY	214	DLVPRPTWOLKAFVFGRRKSRVVDLNLTEEVRLY-----SCPRRFSVSIIBELKRT	266
Dh	1111	DGVEYETPLVG---IY--CGSVLPRTIISHNKKMLKPKSDAALTAKFSA-----	1156
QY	267	DTIWPFGCLLYKRCGNCACCLIHNCBQCVPBSKYTKYHE--VLQIRPTGYRGLHKS	323
Dh	1157	---YWDGGS--STGGCGN---LTPRTGLTSPNYBMPYUHSSECYRLEASHG--SPFELE	1206
QY	324	LTDVALLENHNEEC	335
Dh	1207	FQDFHLEHNPRSC	1218

RESULT 9  
A58788  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human  
N/Alternate names: bone morphogenic protein splice form BMP-1/HIS  
/Species: Homo sapiens (man)

CjDate: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 18-Jun-1999  
CjAccession: A37278; A56788  
RjMowney, J.M.; Rosen, V.; Celeste, A.J.; Mitsuoka, L.M.; Whitters, M.J.; Kriz, R.W.; Hew  
Science 242, 1528-1534, 1998  
Article: Novel regulators of bone formation: molecular clones and activities.  
A.Reference number: A37278; MID:89072730; PMID:3201241

A1:Accession: A31218  
A1:Molecule type: mRNA  
A1:Residues: 1-702, 'ERRPALCPRRGRPHQLKFRVOKNRRTQ,' <MOZ>  
A1:Cross-references: GB:M22489, NID:5179499, PIDN:AA51833.1, PID:g1795000  
R1:Tabakara, K., Lyons, G.E., Greenspan, D.S.  
J. Biol. Chem. 269, 32572-32578, 1994

U-957A: CreM: 5257252576: 1594  
 A>Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded by a single gene  
 A:Reference number: A58788; MUID:95096114; PMID:7798260  
 A:Accession: A58788

A;Molecule type: mRNA  
A;Residues: 703-823 <TAK>  
Accession numbers: CD 135376. NID -G10423. PDB -G10424

A/Cross-References: GB:u332/8; MID:gb0139423; FIDN:AMC41/03.1; FID:gb0139424

A;Gene: GDB:BMPL; BMP-1  
A;Cross-references: GDB:125203; OMIM:112264

A: map position: 8p21-8p21  
C: Function:  
D: Description: cat[urged bird's]uid of the garbow[ terminal] segment id of all]ogen tumor

[illegible]

F:130-321/Domain: astacin homology <AST>  
F:23-823/Product: procollagen C-endopeptidase splice form HIS #stratus predicted <MAT>

F:322-431/Domain: C1r/C1s repeat homology <C1R1>  
F:435-544/Domain: C1r/C1s repeat homology <C1R2>

F:551-587/Domain: EGF homology <EGF>  
F:591-700/Domain: C1r/C1s repeat homology <C1R3>

F:738-752/Region: histidine-rich  
F:91,142,332,365,599/Binding site: carbohydrate (Asn) (covalent) #scatatus predicted

F-2163-319, 185-205, 322-348, 375-397, 435-461, 488-510, 551-565, 555-572, 574-587, 591-617, 644-66  
F-213, 217, 223, 272 Binding site: zinc (His, His, His, Tyr) #status predicted  
E-316/Active site: Cln #status predicted

F7127/Active site: glu #status predicted  
F7565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match .9.3%; Score 173; DB 1; Length 823;  
Best Local Similarity 35.6%; Pred. No. 9.2e-07;

Matches 52; Conservative 19; Mismatches 49; Indels 26; Gaps 7;

Q7 55 NSCSHSRFPHTYPRNTVLYWRLLVA-VEENVMICQTTPDRFGLEDDEDDICKDFFVEEVEE 113  
||| | : ||| : : : |||  
||| | : ||| : : : |||

599 NGSITSPPGPKPEYPNNKNCIQLVAPTOYRISLQDFDPETEG-----NDVCKYDEVEVRS 653

654 GI.TDSKIHGKFGGS - RKPVYITSONNMVEEFSDNYY - SKSGPKAHFFSVI EGAGDRH 711

0Y 172 S-----PSVL-----PPSAL 181

Db 712 SHLSGLELLICPHALVDTVPAPPSAL 737

RESULT 10  
B58788

Alternate names: bone morphogenic protein 1, tollid-like splice form

```
C:\projects\monte_baptista\main
C:\Date: 28-Mar-1998 #sequence revision 09-Apr-1998 #text_change 16-Jul-1999
C:\Accession: A37278 R58788 _
```

R. Woźney, J. M.; Rosen, V.; Celeste, A. J.; Mlotsock, L. M.; Whitters, M. J.; Kriz, R. W.; Hew Science 242, 1528-1534, 1988

A1Title: Novel regulators of bone formation: molecular clones and activities.  
A1Reference number: A37278; MUID:89072730; PMID:3201241

A:Accession: A37278  
A:Molecule type: mRNA

A:Residues: 1-702, 'EKRPALQPPRGPRHQIKFRVQKRNTPQ.' <WZ>  
A:Cross-references: GB:M22488; NID:gl79499; PIDN:AA51833.1; PID:gl79500

Kjidekaido, A.; Lyons, G.E.; Greenberg, D.S.

J. Biol. Chem. 269, 32572-32578, 1994  
 A:Title: Bone morphogenetic protein-1, a mammalian tollid homologue (tm1d) are encod  
 A:Reference number: A58788; MUID:95096114; PMID:7798260  
 A:Accession: B58788  
 A:Molecule type: mRNA  
 A:Residues: 703-966 <TAK>  
 A:Cross-references: GB:L35279; NID:g619860; PIDN:AA61710.1; PID:g619861  
 C:Genetics:  
 A:Gene: GDB:BMP1; BMP-1  
 A:Cross-references: GDB:125203; OMIM:112264  
 A:Map position: 8p21-8p21  
 C:Function:  
 A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type  
 C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; F  
 C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl  
 F:1-22/Domains: signal sequence #status predicted <SIG>  
 F:123-986/Product: procollagen C-endopeptidase tollid-like splice form #status predicted  
 F:130-331/Domains: astacin homology <AST>  
 F:322-431/Domains: C1r/C1s repeat homology <C1R1>  
 F:435-544/Domains: C1r/C1s repeat homology <C1R2>  
 F:551-587/Domains: EGF homology <EG1>  
 F:591-700/Domains: EGF homology <EG2>  
 F:707-742/Domains: C1r/C1s repeat homology <C1R3>  
 F:747-856/Domains: C1r/C1s repeat homology <C1R4>  
 F:860-973/Domains: C1r/C1s repeat homology <C1R5>  
 F:91.142.332.363.599/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:163-319.185-205.322-348.375-387.435-461.488-510.551-563.559-572.574-587.591-617.644-66  
 F:213.217.223.272/Binding site: zinc (His, His, Tyr) #status predicted  
 F:214/Active site: Glu #status predicted  
 F:565.720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.1%; Score 169; DB 1; Length 966;  
 Best Local Similarity 39.4%; Pred. No. 2.6e-06;  
 Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

Qy 55 NGSIHSPFPHTYRNTLVLRVLA-VEENWIOITFDERGLEDPEDDICKYDFVEE 113  
 Db 599 NGSIHSPFPHTYRNTLVLRVLA-VEENWIOITFDERGLEDPEDDICKYDFVEE 113  
 114 --PSDGTILGRWCGSGTVPGKQISKGQIRIRFVSDEYFSPGFCIH 160  
 Db 654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFSDNTV-SKKGFKAHF 700

RESULT 11  
 149540  
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollid-like splice form - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
 C:Accession: 149540  
 R:Rukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.  
 Dev. Biol. 163, 175-183, 1994  
 A:Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel  
 A:Reference number: 149540; MUID:9422342; PMID:8174772  
 A:Accession: 149540  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-991 <RBS>  
 A:Cross-references: GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607  
 C:Genetics:  
 A:Gene: BMP-1  
 C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; F  
 C:Keywords: hydrolyase; metalloproteinase; zinc  
 F:135-346/Domains: astacin homology <AST>  
 F:556-592/Domains: EGF homology <EG1>  
 F:596-705/Domains: C1r/C1s repeat homology <C1R>  
 F:712-747/Domains: EGF homology <EG2>  
 F:218.222.228.277/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F:219/Active site: Glu #status predicted

Query Match 9.1%; Score 169; DB 2; Length 991;  
 Best Local Similarity 39.4%; Pred. No. 2.6e-06;  
 Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

Qy 55 NGSIHSPFPHTYRNTLVLRVLA-VEENWIOITFDERGLEDPEDDICKYDFVEE 113  
 Db 604 NGSIHSPFPHTYRNTLVLRVLA-VEENWIOITFDERGLEDPEDDICKYDFVEE 113  
 114 --PSDGTILGRWCGSGTVPGKQISKGQIRIRFVSDEYFSPGFCIH 160  
 Db 659 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFSDNTV-SKKGFKAHF 705

RESULT 12  
 155362  
 procollagen I C-proteinase enhancer protein precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 05-Nov-1999  
 C:Accession: A55362  
 R:Rukagawa, M.; Kessler, E.; Biniaminov, L.; Bruse, M.; Eddy, R.L.; Jani-Sait, S.; Sho  
 J. Biol. Chem. 269, 26280-26285, 1994  
 A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification,  
 A:Reference number: A55362; MUID:95014462; PMID:7523404  
 A:Accession: A55362  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-449 <TAK>  
 A:Cross-references: GB:L33799; NID:g642907; PIDN:AA61949.1; PID:g642908  
 C:Genetics:  
 A:Gene: GDB:PCOLCE  
 A:Cross-references: GDB:305468; OMIM:600270  
 A:Map position: 7q21.3-7q22  
 C:Superfamily: C1r/C1s repeat homology  
 C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid  
 F:1-25/Domains: signal sequence #status predicted <SIG>  
 F:26-449/Product: #status predicted <MAT>  
 F:37-146/Domains: C1r/C1s repeat homology <C1R1>  
 F:159-270/Domains: C1r/C1s repeat homology <C1R2>  
 F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
 F:29.431/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 154; DB 2; Length 449;  
 Best Local Similarity 33.8%; Pred. No. 1.9e-05;  
 Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;

Qy 56 GSISHPFPHTYRNTLVLRVLA-VEENWIOITFDERGLEDPEDDICKYDFVEE 111  
 Db 168 GSISHPFPHTYRNTLVLRVLA-VEENWIOITFDERGLEDPEDDICKYDFVEE 111  
 112 EEPDGTILGRWCGSGTVPGKQISKGQIRIRFVSDEYFSPGFCIH 168  
 Db 224 AVSDSRIRKFCGD-AVPSISSEGNELVQFSDLSYVAD-GFSASYK-TLPRGTAKE 280

Qy 169 -----EAVSPSY-LPPSALP 182  
 Db 281 GCGPGRKTEPKVLPKPSQP 302

RESULT 13  
 A39288  
 dorsal-ventral patterning protein tollid (EC 3.4.24.-) - fruit fly (Drosophila melanog  
 C:Species: Drosophila melanogaster  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A39288  
 R:Shimell, M.V.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.  
 Cell 67, 469-481, 1991  
 A:Title: The Drosophila dorsal-ventral patterning gene tollid is related to human bone  
 A:Reference number: A39288; MUID:92034970; PMID:1840509  
 A:Accession: A39288  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1057 <SHI>  
 A:Cross-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306  
 C:Genetics:  
 A:Gene: FlyBase:tlid  
 A:Cross-references: FlyBase:FBgn0003719

C/Superfamily: dorsal-ventral patterning protein tollid; astacin homology; C1r/C1s repd  
 C/Keywords: duplication; hydrolase; metalloproteinase; zinc  
 F/136-329/Domain: astacin homology <AST>  
 F/352-464/Domain: C1r/C1s repeat homology <C1R2>  
 F/468-578/Domain: C1r/C1s repeat homology <C1R1>  
 F/585-620/Domain: EGF homology <EG1>  
 F/624-740/Domain: C1r/C1s repeat homology <C1R3>  
 F/747-782/Domain: EGF homology <EG2>  
 F/787-896/Domain: C1r/C1s repeat homology <C1R4>  
 F/900-1013/Domain: C1r/C1s repeat homology <C1R5>  
 F/221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F/222/Active site: Glu #status predicted

## Query Match

Best Local Similarity 8.0%; Score 148.5; DB 1; Length 1057;  
 Matches 38; Conservative 20; Mismatches 35; Indels 7; Gaps 5;

QY 50 ITVSTNGSHSPRPHTYPRNTVLVWRLVAEENWVQLTFDERFGLDEPDIDCKYDFV 109  
 Db 472 LKLTQDSIDSPVPMYDMDKCVWRITR-PDNRQVAKLF-QSFLE--KHGCAVDFV 527

QY 110 EEE--PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 147  
 Db 528 EIRDGNHSDSRLRGFCGDKLPNIK-TRSNQWIRFVSD 566

## RESULT 14

A59271  
 A:Reactive factor (EC 3.4.21.-) 2 precursor - human  
 N/Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)  
 C/Species: Homo sapiens (man)  
 C/Date: 10-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000  
 C/Accession: A59271  
 R/Title: S.; Vorup-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Laursen, S.B.; Poulsen, K.  
 Nature 386, 506-510, 1997  
 A/Title: A second serine protease associated with mannan-binding lectin that activates C  
 A/Reference number: A59271; MUID:97242412; PMID:9087411  
 A/Accession: A59271  
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-686 <JEN>  
 A:Cross-references: GB:Y09926; NID:g4007626; PIDN:CA71059.1; PID:g4007627  
 A:Experimental source: tissue liver  
 A/Note: Submitted to GenBank, December 1996  
 A/Note: parts of this sequence, including the amino end of the mature protein, were dete  
 C/Genetics:  
 A:Gene: GDB:MASP2  
 A:Cross-references: GDB:6071500  
 A/Map position: lp36.2-lp36.3  
 C/Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H  
 C/Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p  
 F/1-15/Domain: signal sequence #status predicted <SIG>  
 F/16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>  
 F/19-134/Domain: C1r/C1s repeat homology <C1R1>  
 F/142-180/Domain: EGF homology <EGF>  
 F/184-293/Domain: C1r/C1s repeat homology <C1R2>  
 F/300-361/Domain: complement factor H repeat homology <FH1>  
 F/366-430/Domain: complement factor H repeat homology <FH2>  
 F/445-679/Domain: trypsin homology <TRY>  
 F/72-90,142-152,167-169,184-211,241-259,300-348,328-361,366-412,396-430,434-552,  
 F/158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 F/444-445/Cleavage site: Arg-116 (autolytic) #status predicted  
 F/483,532/Active site: His, Asp, Ser #status predicted

## Query Match

Best Local Similarity 7.7%; Score 143.5; DB 1; Length 686;  
 Matches 34; Conservative 25; Mismatches 42; Indels 5; Gaps 4;

QY 55 NSGSHSPRPHTYPRNTVLVWRLVAEENWVQLTFDERFGLDEPDIDCKYDFV 114  
 Db 193 SGELSPPEYRPPYKSSCTYS-ISLESGSVLDFESFDVTHPETLCRYDFLKIQ-- 249  
 QY 115 SDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDYFPSEPGCIHY 160

Db 250 TDEEHGPPCGK-TLPHRIETKSNVTITFVDE-SGHTGMKIH 293

## RESULT 15

T31069  
 tollid-BMP-1 like protein 1 - California sea hare  
 N/Alternate names: probable metalloproteinase TBL-1  
 C/Species: Aplysia californica (California sea hare)  
 C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 18-Aug-2000  
 C/Accession: T31069  
 R/Title: Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; B.

U. Neurosci. 17, 735-764, 1997  
 A/Title: A developmental gene (Tollid/BMP-1) is regulated in Aplysia Neurons by treatm  
 A/Reference number: Z20965; MUID:98007484; PMID:8987797  
 A/Accession: T31069  
 A:Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA  
 A/Residues: 1-1070 <LID>  
 A:Cross-references: EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AA47485.1  
 C/Superfamily: dorsal-ventral patterning protein tollid; astacin homology; C1r/C1s repd

## Query Match

Best Local Similarity 7.5%; Score 139.5; DB 2; Length 1070;  
 Matches 70; Conservative 36; Mismatches 102; Indels 11; Gaps 17;

QY 56 GSISHSPRPHTYPRNTVLVWRLVAEENWVQLTFDERFGLDEPDIDCKYDFV 112  
 Db 529 GFLNSPAYDEGSDKVCNM-VITREGVQVLAEPFTFTEF---DPD---CAVDVEIR 581

QY 113 --EPPDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDYFPSEPGCIHY----- 160  
 Db 582 DGGTQDSPLVGYGCGTTR-PPNAISTSRHLVYFVSDSVM-QKGFSSASYLEVDECEGE 639

QY 161 -----NIMWQFTEAVSPSY 175  
 Db 640 DHCCEHVCNTLGSIECTKIGIELHSDGKCEKACGYLDAPSGTISPSF-----PDL 694

QY 176 LPPSALPLDLNNATAPF-----TLEDLIRYLEPERMQLDLEDLYRPTWLLGKAFVG 230  
 Db 695 YPPD-----KNCVHISAPKSHLTITVFTHMLE-WMGDECEL-----DFVRVNVVG 741

QY 231 KRSRVVDLNLLEEVRLYSCTPRNSVS--TEBELKRTDTITWPGCLL-----VKRCGN 283  
 Db 742 NKER-----LOGQYCGFMAPPSITSLNELRIEFRSDTLTKTGFPSMDYVADVOCASS 795

QY 284 CACCLHNCN-----ECOC 296  
 Db 796 NGGCKHICENTVGSFRHCSC 814

Search completed: May 27, 2004, 15:47:22  
 Job time : 15 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: May 27, 2004, 15:38:06 ; Search time 10.5 Seconds  
(without alignments) 1710.877 Million cell updates/sec

Title: US-09-818-943-1  
Perfect score: 1858

Sequence: 1 MSLLFGLLVTSALAGRRGT.....DVLEHHECDVCGRSTNG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179.5	9.7	928	1	NPRL_XENLA
2	176	9.5	707	1	BMP1_XENLA
3	173.5	9.3	616	1	SPAN_STRPV
4	169	9.1	986	1	BMP1_HUMAN
5	169	9.1	991	1	BMP1_MOUSE
6	164.5	8.9	931	1	NPRL_MOUSE
7	163.5	8.8	922	1	NPRL_RAT
8	163	8.8	925	1	NPRL_RAT
9	162.5	8.7	926	1	VEGD_RAT
10	160.5	8.6	923	1	NPRL_MOUSE
11	160.5	8.6	931	1	NPRL_MOUSE
12	159	8.6	1022	1	TLD_MOUSE
13	158.5	8.5	923	1	NPRL_HUMAN
14	157	8.4	914	1	NPRL_CHICK
15	154	8.3	449	1	PCOL_HUMAN
16	148.5	8.0	1057	1	TLD_MOUSE
17	147	7.9	354	1	VEGD_HUMAN
18	143.5	7.7	686	1	MAS2_HUMAN
19	140	7.5	358	1	VEGD_MOUSE
20	139.5	7.5	597	1	BP1_PARLI
21	138.5	7.5	704	1	CRAR_MOUSE
22	138	7.4	639	1	BMPH_STRPV
23	138	7.4	705	1	CRAR_HUMAN
24	137.5	7.4	699	1	CRAR_HUMAN
25	132.5	7.1	3565	1	CSM1_HUMAN
26	132	7.1	419	1	VEGC_HUMAN
27	132	7.1	3564	1	CSM1_MOUSE
28	128	6.9	468	1	PCOL_MOUSE
29	128	6.9	468	1	PCOL_RAT
30	127	6.8	3670	1	CSM3_HUMAN
31	125	6.7	213	1	PDGA_RABIT
32	125	6.7	415	1	VEGC_MOUSE
33	123.5	6.6	277	1	TSG6_HUMAN

## ALIGNMENTS

RESULT 1	ID	NPRL_XENLA	STANDARD	PRT	928 AA.
AC	P28824				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Neuropilin-1 precursor (A5 protein) (A5 antigen).				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;				
OC	Xenopodidae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=91337458; PubMed=1908252;				
RA	Takagi S., Hirata T., Agata K., Mochi M., Eguchi G., Fujisawa H.;				
RT	"The A5 antigen, a candidate for the neuronal recognition molecule, has homologies to complement components and coagulation factors.";				
RL	Neuron 7:235-307(1991).				
CC	- FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepulsive activity of semaphorins (By similarity). Presumed to be involved in the neuronal recognition between the optic nerve fibers and the visual centers.				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- TISSUE SPECIFICITY: Retinal ganglion cells and visual center neurons.				
CC	- SIMILARITY: Belongs to the neuropilin family.				
CC	- SIMILARITY: Contains 2 CUB domains.				
CC	- SIMILARITY: Contains 2 F5/8 type C domains.				
CC	- SIMILARITY: Contains 1 MAM domain.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb.ch/announce/">http://www.isb.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	EMBL: D10467; BAA01260.1; ..				
DR	HSSP; P12259; 1CZT.				
DR	InterPro; IPR000859; CUB.				
DR	InterPro; IPR000421; FAS5.C.				
DR	InterPro; IPR008979; Gal Bind like.				
DR	InterPro; IPR000998; MAM_domain.				
DR	Pfam; PF00431; CUB; 2.				
DR	Pfam; PF00754; F5_F8_type_C; 2.				
DR	Pfam; PF00629; MAM; 1.				
DR	PRINTS; PR00020; MAMDOMAIN.				
DR	SMART; SM00042; CUB; 2.				
DR	SMART; SM00231; FAS5C; 2.				
DR	SMART; SM00137; MAM; 1.				

34	122	6.6	3487	1	CSM2_HUMAN	Q7408 homo sapien
35	120.5	6.5	245	1	PDGB_FELCA	P12919 felis silve
36	120.5	6.5	275	1	TSG6_MOUSE	O08859 mus musculu
37	118.5	6.4	276	1	TSG6_RABIT	P98069 oryctolagus
38	114.5	6.2	148	1	VEGH_ORFN7	P52585 orf virus (
39	114.5	6.2	241	1	PDGB_HUMAN	P01127 homo sapien
40	112.5	6.1	226	1	PDGA_XENLA	P13698 xenopus lae
41	111.5	6.0	514	1	IYV2_XENLA	P42664 xenopus lae
42	110	5.9	211	1	PDGA_MOUSE	P20033 mus musculu
43	109	5.9	204	1	PDGA_RAT	P28576 rattus norv
44	108.5	5.8	164	1	VEGA_CAVPO	P26617 cavia porce
45	108.5	5.8	226	1	TSIS_SMSAV	P01128 simian sarc

```

DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FASEC_1; 2.
DR PROSITE; PS01286; FASEC_2; 2.
DR PROSITE; PS50022; FASEC_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neutrone; Signal; Repeat;
KM Receptor; Antigen.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 928 NEUROPILIN-1.
FT DOMAIN 22 860 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 861 883 POTENTIAL.
FT DOMAIN 884 928 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 584 F5/8 TYPE C 2.
FT DOMAIN 646 812 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 584 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 844 844 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 928 AA; 103416 MW; AF68323B0A4C789D CRC64;

Query Match 9.7%; Score 179.5; DB 1; Length 928;
Best Local Similarity 31.6%; Pred. No. 2,2e-07;
Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;

QY 50 ITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQLTFDEFGLEDEDDICKYDFV 109
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 31 IKITSPSYLTSAQPHSPSPSCRMILQAPHYQRIMINPHFLEDEB--CKDYV 87
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 110 EV--EESPDGTTIGRMCGSGTVPKQSKNGNQRIRVSPSEYPSSEPGFIHNIYWP-- 155
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 88 EVIDGDANGQLGKCYGK-IAPSPVSTSPSIFIRVSDYETPG-AGFSIRYEVKTPG 145
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 166 ----QETEA--VSPSVLPSPALPLDLINATFSTLEDDIRYLEPERMQLDLE 213
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 146 ECSRNFSSNGVILKSPKYPEKYNALACTYIIIPAPKQELV--LFFSFLLEAD 197
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 2
BMP1_XENLA STANDARD; PRT; 707 AA.
ID BMP1_XENLA
AC P98070;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DR Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94085787; PubMed=8262384;
RA Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
RT "Cloning and expression of cDNA encoding Xenopus laevis bone
morphogenetic protein-1 during early embryonic development.";
RL Gene 134:257-261(1993).
CC -!- FUNCTION: Involved in pattern formation in gastrula and later
CC differentiation of developing organs.
CC -!- DEVELOPMENTAL STAGE: Blastula, early gastrula and hatched
CC tadpoles; little or no expression in morula and late gastrula.

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CC -!- SIMILARITY: Belongs to peptidase family M12a.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 3 CUB domains.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC -----
CC EMBL; L12249; AAA16313.1; -.
CC PIR; J02218; J02218.
CC HSSP; P00736; IAPQ.
CC MEROPS; M12_005; -.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12a.
DR Pfam; PF01400; CUB; 3.
DR Pfam; PF00431; CUB; 3.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 3.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00235; ZMNG; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS00022; EGF_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;
KW Hydrolyase; Protease; Metalloprotease; EGF-like domain; Zinc; Calcium;
KW Signal.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP ? 83 POTENTIAL.
FT CHAIN 84 707 BONE MORPHOGENETIC PROTEIN 1.
FT DOMAIN 84 284 METALLOPROTEASE.
FT DOMAIN 285 397 CUB 1.
FT DOMAIN 398 509 CUB 2.
FT DOMAIN 510 551 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 554 666 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 176 176 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 177 177 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 180 180 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 186 186 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 146 149 BY SIMILARITY.
FT DISULFID 514 526 BY SIMILARITY.
FT DISULFID 522 535 BY SIMILARITY.
FT DISULFID 537 550 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC98BD CRC64;

Query Match 9.5%; Score 176; DB 1; Length 707;
Best Local Similarity 43.3%; Pred. No. 3.1e-07;
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

QY 55 NSGISPRPHYPRNTVLVWRLVAEENWVQLTFDEFGLEDEDDICKYDFVEE- 113
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 562 NSGISPGFKXPYPRKNCITQVLVAPQ-YRISLFDQ--FETGNDVCKTDFAVRSRG 617
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 114 -PSDGTILGRMGSGTVPKQSKNGNQRIRVSPSEYPSSEPGF 156
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```



[4]  
PARTIAL SEQUENCE FROM N.A. (ISOFORMS Bmp1-3 AND Bmp1-7).  
TISUSe=Placenta; PubMed=7798260;  
MEDLINE=95096114;  
Takehara K., Lyons G.E., Greenspan D.S.;  
"Bone morphogenetic protein-1 and a mammalian tollid homologue (mtld)  
are encoded by alternatively spliced transcripts which are  
differentially expressed in some tissues."  
J. Biol. Chem. 269:32572-32578(1994).  
[5]  
DISULFIDE BOND IN METALLOPROTEINASE DOMAIN.  
MEDLINE=21336528; PubMed=11283002;  
Garrigue-Anlar L., Barker C., Kadler K.E.;  
"Identification of amino acid residues in bone morphogenetic  
protein-1 important for procollagen C-proteinase activity."  
J. Biol. Chem. 276:26233-26242(2001).  
- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II  
and III. Induces cartilage and bone formation.  
- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at  
Ala-I-Asp in type I and II procollagens and at Arg-I-Asp in type  
III.  
- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
- ENZYME REGULATION: Activity is increased by the procollagen C-  
enzymepeptidase enhancer protein.  
- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=7;  
Name=Bmp1-3;  
IsoId=P13497-1; Sequence=Displayed;  
Name=Bmp1-1;  
IsoId=P13497-2; Sequence=VSP\_005461, VSP\_005462;  
Name=Bmp1-2;  
IsoId=P13497-7; Sequence=Not described;  
Name=Bmp1-4;  
IsoId=P13497-3; Sequence=VSP\_005463, VSP\_005464;  
Name=Bmp1-5;  
IsoId=P13497-4; Sequence=VSP\_005465, VSP\_005466;  
Name=Bmp1-6;  
IsoId=P13497-5; Sequence=VSP\_005467, VSP\_005468;  
Name=Bmp1-7;  
IsoId=P13497-6; Sequence=VSP\_005469, VSP\_005470;  
- TISSUE SPECIFICITY: Ubiquitous.  
- SIMILARITY: Belongs to peptidase family M12A.  
- SIMILARITY: Contains 2 EGF-like domains.  
- SIMILARITY: Contains 5 CUB domains.  
-----  
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or send an email to [license@isb.ch](mailto:license@isb.ch)).  
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EMBL; U50330; AAA93462.1; -  
EMBL; M22488; AAA51833.1; -  
EMBL; Y08723; CAA69973.1; -  
EMBL; Y08724; CAA69974.1; -  
EMBL; Y08725; CAA69975.1; -  
EMBL; L35278; AAC41703.1; -  
EMBL; L35279; AAC41710.1; -  
PIR; A37278; B58788.  
DR HSSP; P00736; IAPQ.  
DR MEROPS; M2.005; -  
DR Genew; HGNC:1067; Bmp1.  
MIM; 11264; -  
GO; GO:0005576; C:extracellular; NAS.  
GO; GO:000823; F:metallopeptidase activity; NAS.  
GO; GO:0001502; P:cartilage condensation; TAS.  
GO; GO:0007275; P:development; TAS.  
InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR001881; EGF\_Ca.  
InterPro; IPR006209; EGF\_like.

DR		InterPro:	IPR006025;	PepT_M Zn_BS.
DR		InterPro:	IPR006026;	Peptidase_M.
DR		InterPro:	IPR001506;	Peptidase_M1ZA.
DR		Pfam:	PF01400;	Astacin; 1.
DR		Pfam:	PF00431;	CUB; 5.
DR		Pfam:	PF00008;	EGF; 2.
DR		PRINTS:	PR00480;	ASTACIN.
DR		SMART:	SM00042;	CUB; 5.
DR		SMART:	SM00179;	EGF_CA; 2.
DR		SMART:	SM00235;	ZnMG; 1.
DR		PROSITE:	PS00010;	ASX_HYDROXYL; 2.
DR		PROSITE:	PS01180;	CUB; 5.
DR		PROSITE:	PS00022;	EGF_1; FALSE_NEG.
DR		PROSITE:	PS01186;	EGF_2; 2.
DR		PROSITE:	PS50026;	EGF_3; 2.
DR		PROSITE:	PS01187;	EGF_CA; 2.
DR		Growth factor:	CSO0142;	ZINC_PROTEASE; 1.
KW		Osteoclast:	OCCLASSTC;	Chondrogenesis;
KW		Osteoblast:	OSTEOBLASTC;	Chondrogenesis;
KW		Hydrolase:	METALLOPROTEIN_C;	Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KM		Glycoprotein:	ZYMOTENIN;	Alternative splicing.
FT	SIGNAL	1	22	POTENTIAL.
FT	PROPEP	23	120	POTENTIAL.
FT	CHAIN	121	986	BONE MORPHOGENETIC PROTEIN 1.
FT	DOMAIN	121	321	METALLOPROTEASE.
FT	DOMAIN	322	434	CUB 1.
FT	DOMAIN	435	546	CUB 2.
FT	DOMAIN	547	588	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	591	743	CUB 3.
FT	DOMAIN	704	743	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	747	859	CUB 4.
FT	DOMAIN	860	976	CUB 5.
FT	METAL	213	213	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT_SITE	214	214	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	217	217	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	223	223	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISULFID	183	186	BY SIMILARITY.
FT	DISULFID	322	348	BY SIMILARITY.
FT	DISULFID	375	397	BY SIMILARITY.
FT	DISULFID	435	461	BY SIMILARITY.
FT	DISULFID	488	510	BY SIMILARITY.
FT	DISULFID	551	563	BY SIMILARITY.
FT	DISULFID	559	572	BY SIMILARITY.
FT	DISULFID	574	587	BY SIMILARITY.
FT	DISULFID	591	617	BY SIMILARITY.
FT	DISULFID	644	666	BY SIMILARITY.
FT	DISULFID	707	718	BY SIMILARITY.
FT	DISULFID	714	727	BY SIMILARITY.
FT	DISULFID	729	742	BY SIMILARITY.
FT	CARBOHYD	91	91	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	363	363	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	599	599	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	VARSPLIC	703	730	DDEDSKNGSGQDDCVNTPSYEQQR -> EKRPALQPPRRPQLKFRVOKNRITQ (in isoform BMP1-1).
FT				/FTId=VSP 005461.
FT	VARSPLIC	731	986	Missing (in isoform BMP1-1).
FT				/FTId=VSP 005462.
FT	VARSPLIC	245	302	DEVNLKNKEPOEVESLGTFYDFDSIMHYARTSRGIFLDTDIYPKYENVAYKVPISIGR -> VHHSSLLSLSCGRNASFPCLSBSSTHQALCWTLGLFLRPSPFFRLPLAARTLRAGV (in isoform BMP1-4).
FT				/FTId=VSP 005463.
FT	VARSPLIC	303	986	Missing (in isoform BMP1-4).
FT				/FTId=VSP 005464.
FT	VARSPLIC	589	622	AACGGFTLKINGSITSPEWKERYPPNNKCIVOLV -> GCYLQVKPKPLMDRHCFERLSHTGEMLGTALRG (in isoform BMP1-5).
FT				/FTId=VSP 005465.
FT	VARSPLIC	623	986	Missing (in isoform BMP1-5).
FT				/FTId=VSP 005466.
FT	VARSPLIC	703	717	DDEDSKNGSGQQD -> GGELFGLLGHPPRRP (in isoform BMP1-6).



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FT  /FtId=VSP_005467.
FT  Missing (in isoform BMP1-6).
FT  /FtId=VSP_005468.
FT  VARSPLIC 718 986
FT  VARSPLIC 703 823
FT  DKECSKDNCGCCODCVNTPSYSCQCRSGFVLDNRKDC
FT  EAGCDHKVTSIGTITSNWPDKTPSKKECTWALSIFGR
FT  VKLTFMEWDIESQECADYDLFVDPGRAPVIGRFG
FT  -> VLEGAGDRSHSLGIELLCPLALVTPAPPSALHGD
FT  THAHTHTVHTHCPVIAOETGCRPLASRLSPQSGHLLTA
FT  PQEGSYLDPMTHRGDPKRRRRRSIKTFSITPFRGIMA
FT  L (in isoform BMP1-7).
FT  /FtId=VSP_005469.
FT  Missing (in isoform BMP1-7).
FT  VARSPLIC 824 986
FT  /FtId=VSP_005470.
FT  CONFLICT 748 748
FT  CONFLICT 934 934
FT  R -> N (IN REF. 4).
FT  R -> S (IN REF. 4).
SQ  SEQUENCE 986 AA; 111248 MW; F89201913AC3CBB4 CRC64;

Query Match 9.1%; Score 169; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 1.9e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

Qy 55 NGSHSRPFHTYPRNTVLVRLVA--VEENVWITLTFDERFGLDEPDDICKDFVEVEE 113
Db 599 NGSITSGWPKPEYPPNNKNCIMQVAPVQYRISLQDFEFETG-----NDVCKYDFVEVRS 653
Qy 114 --PSDGTILGRMGSGTVPGKQISKGNQIRIRFVSEDFEPEPCFIHY 160
Db 654 GLTADSKLHGKFCOS-EKPEVITSQNNWVRFESDNTV-SKKGPKAHF 700

RESULT 5
BMP1_MOUSE
ID _BMP1_MOUSE STANDARD; PRT; 991 AA.
AC P98063;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
DE (Procollagen C-proteinase) (PCP) (Mammalian tollold protein) (mtld).
GN BMP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RX MEDLINE=94229342; PubMed=8174772;
RA Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
RT "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT which is related to the Drosophila dorsoventral gene tollold and
RT encodes a putative astacin metalloendopeptidase."
RL Dev. Biol. 163:175-183(1994).
CC -1- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
CC and III. Induces cartilage and bone formation.
CC -1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala-I-Asp in type I and II procollagens and at Arg-I-Asp in type
CC III.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- ENZYME REGULATION: Activity is increased by the procollagen C-
CC endopeptidase enhancer protein.
CC -1- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
CC and floor plate region of the neural tube. Less in developing
CC membranes and endochondral bone, submucosa of intestine, dermis
CC of skin and the mesenchyme of spleen and lung.
CC -1- SIMILARITY: Belongs to peptidase family M12A.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -1- SIMILARITY: Contains 5 CUB domains.
CC -----
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CC -----
CC EMBL; L24755; AAA37306.1; -.
CC PIR; I49540; I49540.
CC HSSP; P00736; IAPQ.
CC MEROPS; M12.005; -.
CC MGD; MGI:88176; Bmp1.
DR InterPro; IPR000152; Aex_hydroxyl_5.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006025; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;
KW Hydrolyase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KM Glycoprotein; Zymogen.
FT SIGNAL 1 25
FT PROPEP 26 125
FT CHAIN 126 991
FT DOMAIN 126 326
FT DOMAIN 327 439
FT DOMAIN 440 551
FT DOMAIN 552 593
FT DOMAIN 596 707
FT DOMAIN 708 748
FT DOMAIN 752 864
FT DOMAIN 865 981
FT METAL 218 218
FT ACT_SITE 219 219
FT METAL 222 222
FT METAL 228 228
FT DISULFID 188 191
FT DISULFID 327 353
FT DISULFID 380 402
FT DISULFID 440 466
FT DISULFID 493 515
FT DISULFID 556 568
FT DISULFID 564 577
FT DISULFID 579 592
FT DISULFID 596 622
FT DISULFID 649 671
FT DISULFID 712 723
FT DISULFID 719 732
FT DISULFID 734 747
FT CARBOHYD 96 96
FT CARBOHYD 147 147
FT CARBOHYD 337 337
FT CARBOHYD 368 368
FT CARBOHYD 604 604
SQ SEQUENCE 991 AA; 111607 MW; 68A1847783A0BB9E CRC64;

Query Match 9.1%; Score 169; DB 1; Length 991;
Best Local Similarity 39.4%; Pred. No. 1.9e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

Qy 55 NGSHSRPFHTYPRNTVLVRLVA--VEENVWITLTFDERFGLDEPDDICKDFVEVEE 113

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Db      604 NGSTSPGMPKPEYPPNKNCIMQVLVAPFYRLSTLQDFPFTG5-----NDVCKYDPEVRS 658
Oy      114 --PSNGTILGRMCGSGTVPKGOISKGNQIRIRFVSDEFPSPEPCITY 160
Db      659 GLTADSKLHGKFCGS-EKPEYITSGYNMRYEFSKSDTV-SKKGFKAHF 705

RESULT 6
NRP2_HUMAN NRP2_HUMAN STANDARD; PRT; 931 AA.
AC O60462; O14820; O14821;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neupophilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
GN NRP2 OR VEGF165R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
RX MEDLINE=97470888; PubMed=9331348;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neupophilin-2, a novel member of the neupophilin family, is a high
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema
RT III."
RL Neuron 19:547-559 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A22).
RP TISSUE=Breast;
RC MEDLINE=98180809; PubMed=9529250;
RX Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.;
RA "Neupophilin-1 is expressed by endothelial and tumor cells as an
RT isoform-specific receptor for vascular endothelial growth factor.";
RL Cell 92:735-745 (1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=20309748; PubMed=10748121;
RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neupophilin-2 and neupophilin-1 are receptors for the 165-amino acid
RT form of vascular endothelial growth factor (VEGF) and of placenta
RT growth factor-2, but only neupophilin-2 functions as a receptor for
RT the 145-amino acid form of VEGF."
RL J. Biol. Chem. 275:18040-18045 (2000).
CC -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165
CC and VEGF-145 isoforms of VEGF, and the p16g-2 isoform of p6g.
CC -1- SUBUNIT: Neupophilin-2 probably forms a heterometric complex with
CC neupophilin-1 in order to be a functional semaphorin 3C receptor.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=A22;
CC IsoId=O60462-1; Sequence=Displayed;
CC Name=A0;
CC IsoId=O60462-2; Sequence=VSP_004342;
CC Name=A17;
CC IsoId=O60462-3; Sequence=VSP_004341;
CC -1- SIMILARITY: Belongs to the neupophilin family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC
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DB	Query Match	Best Local Similarity	Matches	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score</
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RESULT 7
NRPL_RAT ID NRPL_RAT STANDARD: PRT: 922 AA.
AC Q90W09;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).
GN NRPL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RT "Neuropilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -1- FUNCTION: Receptor involved in the development of the
CC cardiovascular system, in angiogenesis, in the formation of
CC certain neuronal circuits and in organogenesis outside the nervous
CC system. It mediates the chemorepellant activity of semaphorins. It
CC binds to semaphorin 3A, the PLGF-2 isoform of RGF, the VEGF-165
CC isoform of VEGF and VEGF-B. Coexpression with KDR results in
CC increased VEGF-165 binding to KDR as well as increased chemotaxis.
CC It may regulate VEGF-induced angiogenesis (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Found in the embryonic nervous system.
CC -1- SIMILARITY: Belongs to the neuropilin family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
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CC -----
DR EMBL; AF016296; AAC53337.1; -.
DR HSSP; P12259; IC2T.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR008979; Gal_Bind_Like.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR PRINTS; PRO0020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS8C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01285; FAS8C_1; 2.
DR PROSITE; PS01286; FAS8C_2; 2.
DR PROSITE; PS00222; FAS8C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00600; MAM_2; 1.
DR PROSITE; PS00600; MAM_2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor.
FT CHAIN 1 21 POTENTIAL.
FT DOMAIN 22 922 NEUROPILIN-1.
FT TRANSMEM 22 855 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 856 880 POTENTIAL.
FT DOMAIN 881 922 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.

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FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.
FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 922 AA; 103082 MW; CC6F82AD09B0F2E CRC64;

Query Match 8.8%; Score 163.5; DB 1; Length 922;
Best Local Similarity 36.5%; Pred. No. 5.1e-06;
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;

QY 50 ITVSTNGSIHSPRPPTYPRNTVLWRLVAEENWVLTQTFDERPGLDEPDDICTKDFV 109
DB 31 IKIENPGYLSPGYPHSYSEKCEWLIQAEPEYQRIIMINFPHFLEDRD---CKYDYV 87
QY 110 EV--EPPSDGTLGRMCGSGTVPGKOISKQNIIRFPVSDYFSEPGFCIHNYI 162
DB 88 EVIDENEGKRLWGRKFCCK-IAPSPVSSGFLPIKIFVSD-YETHGAGFSIRYEI 140

RESULT 8
NRPL_RAT ID NRPL_RAT STANDARD: PRT: 925 AA.
AC Q35276;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
GN NRPL2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RT "Neuropilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165
CC and VEGF-145 isoforms of VEGF, and the PLGF-2 isoform of RGF.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Found in certain neuronal populations of the
CC CNS and in other nonneuronal tissues including mesenchymal tissue
CC lining in the ribs.
CC -1- SIMILARITY: Belongs to the neuropilin family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -----
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CC -----
DR EMBL; AF016297; AAC53338.1; -.
DR HSSP; P12259; IC2T.
DR InterPro; IPR000859; CUB.

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DR InterPro; IPR000421; FASB\_C.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR000998; MAM\_domain.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00754; F5\_F8\_type\_C; 2.  
 DR Pfam; PF00629; MAM; 1.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00231; FASB\_C; 2.  
 DR SMART; SM00137; MAM; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01285; FASB\_C; 2.  
 DR PROSITE; PS01286; FASB\_C; 2.  
 DR PROSITE; PS50022; FASB\_C; 2.  
 DR PROSITE; PS50060; MAM; 2; 1.  
 DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.  
 FT SIGMUL 1 22  
 FT CHAIN 23 925  
 FT DOMAIN 23 858  
 FT TRANSMEM 859 883  
 FT DOMAIN 884 925  
 FT DOMAIN 28 142  
 FT DOMAIN 149 267  
 FT DOMAIN 277 427  
 FT DOMAIN 434 592  
 FT DOMAIN 642 802  
 FT DISULFID 28 55  
 FT DISULFID 83 105  
 FT DISULFID 149 175  
 FT DISULFID 208 230  
 FT DISULFID 277 427  
 FT DISULFID 434 592  
 FT CARBOHYD 152 152  
 FT CARBOHYD 157 157  
 FT CARBOHYD 629 629  
 FT CARBOHYD 833 833  
 FT CARBOHYD 834 834  
 SQ SEQUENCE 925 AA; 103896 MW; 3BF62903F644851C CRC64;

Query Match 8.8%; Score 163; DB 1; Length 925;  
 Best Local Similarity 33.8%; Pred. No. 5.6e-06;  
 Matches 45; Conservative 20; Mismatches 60; Indels 8; Gaps 5;

QY 32 PSSNKGQNGVQDQHERITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMIOITPD 91  
 DB 15 FSGHAKYS-QDDPCGGRLNSKDAGYITSPGYQDPSHNCGMVVYAPENQKIVLNFN 73  
 QY 92 EREGLEDPEDDICKYDFVEVE--EPSPDGLTGERKCGSGIVYKQIKGNOIRIRFVSDEX 149  
 DB 74 PHEIEKHND---CKYDFIEIRDDSDSADLKGKCGN-IAPPTLISSGSVLYIKFTSD-Y 128  
 QY 150 FPEPGEFCIHNI 162  
 DB 129 ARQAGAFSLRYEI 141

RESULT 9  
 VEGD RAT STANDARD; PRT; 326 AA.  
 AC 035251;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FtGF).  
 GN FtGF OR VEGFD.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;

RA Yamada Y., Hirata Y., Nezu J., Shitane M.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (Flt4) receptor (By similarity).  
 CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDS) bound by non-covalent interactions (By similarity).  
 CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.  
 CC -----  
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 CC -----  
 DR EMBL; AF014827; AAB66557.1; -.  
 DR HSSP; P15692; 1VPP.  
 DR InterPro; IPR004153; CXKCX repeat.  
 DR InterPro; IPR000072; PD\_growth\_factor.  
 DR Pfam; PF03128; CXKCX; 1.  
 DR Pfam; PF00341; PDGF; 1.  
 DR ProDom; PD001629; PD\_growth\_factor; 1.  
 DR SMART; SM00441; PDGF; 1.  
 DR PROSITE; PS00249; PDGF\_1; 1.  
 DR PROSITE; PS0278; PDGF\_2; 1.  
 DR Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.  
 FT SIGMUL 1 21  
 FT PROPEP 22 93  
 FT CHAIN 94 210  
 FT PROPEP 211 326  
 FT DOMAIN 227 317  
 FT REPEAT 227 242  
 FT REPEAT 263 278  
 FT REPEAT 282 298  
 FT REPEAT 306 317  
 FT DISULFID 116 158  
 FT DISULFID 147 194  
 FT DISULFID 151 196  
 FT DISULFID 141 141  
 FT DISULFID 150 150  
 FT CARBOHYD 160 160  
 FT CARBOHYD 190 190  
 FT CARBOHYD 292 292  
 SQ SEQUENCE 326 AA; 37112 MW; 1261AF373596C00 CRC64;

Query Match 8.7%; Score 162.5; DB 1; Length 326;  
 Best Local Similarity 30.0%; Pred. No. 1.6e-06;  
 Matches 61; Conservative 23; Mismatches 80; Indels 39; Gaps 9;

QY 155 GSCIHNIYMPQTEVSSVLPSPALPDLNNAITASTLEDLRILEPPEWQDLED 214  
 DB 21 GSIEHRAVKVDSLESSRSVLERS-----EQQIRASTLEELLQVAHSDWK----- 68  
 QY 215 IYRPTWOLGKAFVGRKSR-----VVDNLTEVRRLYSCTPRNFVSIRRE 262  
 DB 69 IWRCRKLKSLANDVSRSTSHSTRPAFTYDTETLKVIDEMQRQCSPREVCVASE 128  
 QY 263 L-KRTDTIFWPGCLLVKRCGNCACCLHNCNCCQV---PSKYTKYHEVLIQLRPTGYR 318

```

Db      129 LGKTTNTEFFKPCVCNVPFCGG---CC--NBSVMCMNTSTVSIHQLEBISV--PLTSV- 180
Qy      319 GLHKSLTVDVALEHHEECDCVCG 341
          | : | | | | |
Db      181 ---PELVVPKIANHMGCKCLPTG 200

RESULT 10
ID      NRPI_MOUSE      STANDARD;      PRT;      923 AA.
AC      P97333;
DR      01-NOV-1997 (Rel. 35, Created)
DR      01-NOV-1997 (Rel. 35, Last sequence update)
DR      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Neupilin-1 precursor (A5 protein).
GN      NRPI OR NRPI.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
OX      NCBI_Taxid=10090;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c; TISSUE=Embryonic brain;
RX      MEDLINE=96553149; PubMed=8748368;
RA      Kawakami A., Kiteukawa T., Takagi S., Fujisawa H.;
RT      "Developmentally regulated expression of a cell surface protein,
RT      neupilin, in the mouse nervous system.";
RL      J. Neurobiol. 29:1-17(1996).
CC      -1- FUNCTION: Receptor involved in the development of the
CC      cardiovascular system, in angiogenesis, in the formation of
CC      certain neuronal circuits and in organogenesis outside the nervous
CC      system. It mediates the chemorepulsant activity of semaphorins. It
CC      binds to semaphorin 3A, the pLGF-2 isoform of PGF, the VEGF-165
CC      isoform of VEGF and VEGF-B. Coexpression with KDR results in
CC      increased VEGF-165 binding to KDR as well as increased chemotaxis.
CC      It may regulate VEGF-induced angiogenesis (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- TISSUE SPECIFICITY: Nervous system.
CC      -1- SIMILARITY: Belongs to the neupilin family.
CC      -1- SIMILARITY: Contains 2 CUB domains.
CC      -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC      -1- SIMILARITY: Contains 1 MAM domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.ebi.ac.uk/announcements
CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL; D50086; BAA08789.1; -.
DR      HSSP; P12259; ICGT.
DR      MGD; MGI:106206; Nrp.
DR      GO; GO:0017154; F:semaphorin receptor activity; IGI.
DR      InterPro; IPR000859; CUB.
DR      InterPro; IPR000421; FAS8_C.
DR      InterPro; IPR008979; Gal Bind like.
DR      InterPro; IPR000998; MAM_domain.
DR      Pfam; PF00431; CUB; 2.
DR      Pfam; PF00754; F5_F8_type_C; 2.
DR      Pfam; PF00629; MAM; 1.
DR      PRINTS; PR00020; MAMDOMAIN.
DR      SMART; SMO0042; CUB; 2.
DR      SMART; SMO0231; FAS8C; 2.
DR      SMART; SMO0137; MAM; 1.
DR      PROSITE; PS01180; CUB; 2.
DR      PROSITE; PS01285; FAS8C_1; 2.
DR      PROSITE; PS01286; FAS8C_2; 2.
DR      PROSITE; PS50022; FAS8C_3; 2.
DR      PROSITE; PS00740; MAM_1; 1.
DR      PROSITE; PS50060; MAM_2; 1.
DR      PROSITE; PS50060; MAM_2; 1.
DR      Angiogenesis; Transmembrane; Glycoprotein; Neurone; signal; Repeat;

```

KM Receptor.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 923 NEUROFILIN-1.  
 FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 857 879 POTENTIAL.  
 FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 27 141 CUB 1.  
 FT DOMAIN 147 265 CUB 2.  
 FT DOMAIN 275 424 F5/8 TYPE C 1.  
 FT DOMAIN 431 583 F5/8 TYPE C 2.  
 FT DOMAIN 645 811 MAM.  
 FT DISULFID 27 54 PROBABLE.  
 FT DISULFID 82 104 PROBABLE.  
 FT DISULFID 147 173 PROBABLE.  
 FT DISULFID 206 228 PROBABLE.  
 FT DISULFID 275 424 BY SIMILARITY.  
 FT DISULFID 411 583 BY SIMILARITY.  
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 842 842 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 923 AA; 103020 MW; 06448BA170796808 CRC64;  
  
 Query Match 8.6%; Score 160.5; DB 1; Length 923;  
 Best Local Similarity 36.5%; Pred. No. 9.2e-06;  
 Matches 42; Conservative 16; NoMatches 50; Indels 7; Gaps 4  
  
 QY 50 ITVSTNGSIHSRPHTYPRMTVLWRLVAEENVIQLTDPERGLDEPDIDCKYDPV 109  
 DB 31 IKIENPGVLTSDGYSHYPSBKCKWLIQAPPEYRRIINFPHELEBRD--CKYD 87  
 QY 110 EV--EESPDTGTLIGRCGSGTVPKQISKGNDIRIRFVSDYFSPSPGFCIHVNI 162  
 DB 88 EVIDENNGGRMGKFCCK-IAPSPVVS GPEPLPIKFPDSD-YETGAGFSRIYEI 140  
  
 Db EVIDENNGGRMGKFCCK-IAPSPVVS GPEPLPIKFPDSD-YETGAGFSRIYEI 140  
  
 RESULT 11  
 NRP2\_MOUSE  
 ID NRP2\_MOUSE STANDARD: PRT: 931 AA.  
 AC 035375; 035373; 035374; 035376; 035377; 035378;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165  
 receptor 2).  
 GN NRP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).  
 RC STRAIN=BALB/c.  
 RA MEDLINE=97470889; PubMed=9331348;  
 RX Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
 RT "Neuropilin-2, a novel member of the neuropilin family, is a high  
 RT affinity receptor for the semaphorins Sema B and Sema IV but not Sema  
 RT III.";  
 RL Neuron 19:547-559(1997).  
 CC -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165  
 CC and VEGF-145 isoforms of VEGF, and the pLGF-2 isoform of PGF.  
 CC -1- SUBUNIT: Neuropilin-2 probably forms a heteromeric complex with  
 CC neuropilin-1 in order to be a functional semaphorin B receptor.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=6;  
 CC Name=A22;  
 CC IsoId=035375-1; Sequence=Displayed;  
 CC Name=A0;  
 CC IsoId=035375-2; Sequence=VSP\_004344;  
 CC Name=A5;  
 CC IsoId=035375-3; Sequence=VSP\_004345;  
 CC

CC	Name=A17;
CC	- IsoId=OJ35375-4; Sequence=VSP_004343;
CC	Name=B0;
CC	- IsoId=OJ35375-5; Sequence=VSP_004346;
CC	Name=B5;
CC	- IsoId=OJ35375-6; Sequence=VSP_004347;
CC	- TISSUE SPECIFICITY: Expressed in developing cns, PNS and in some nonneural tissues including limb buds, developing bones, muscles, intestinal epithelium, kidney, lung and submandibular gland.
CC	- DEVELOPMENTAL STAGE: The expression pattern is very dynamic and is developmentally regulated.
CC	- SIMILARITY: Belongs to the neurofilin family.
CC	- SIMILARITY: Contains 2 CUB domains.
CC	- SIMILARITY: Contains 1 F5/8 type C domains.
CC	- SIMILARITY: Contains 1 MAM domain.
CC	-----
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CC	-----
DR	EMBL; AF022856; AAC53379.1; -
DR	EMBL; AF022854; AAC53377.1; -
DR	EMBL; AF022855; AAC53378.1; -
DR	EMBL; AF022857; AAC53380.1; -
DR	EMBL; AF022858; AAC53381.1; -
DR	EMBL; AF022861; AAC53382.1; -
DR	HSSP; P12259; ICZT.
NR	MGD; MG1.I100492; NRP2.
DR	InterPro; IPR000859; CUB.
DR	InterPro; IPR000421; FA5B_C.
DR	InterPro; IPR008979; Gal_bind_like.
DR	InterPro; IPR000998; MAM_domain.
DR	Pfam; PF00431; CUB; 2.
DR	Pfam; PF00754; PS_F8_type_C; 2.
DR	Pfam; PF00629; MAM; 1.
DR	PRINTS; PR00020; MAMDOMAIN.
DR	SMART; SMO0042; CUB; 2.
DR	SMART; SMO0137; FA5B_C; 2.
DR	SMART; SMO0137; MAM; 1.
DR	PROSITE; PS01180; CUB; 2.
DR	PROSITE; PS01285; FA5B_C_1; 2.
DR	PROSITE; PS01286; FA5B_C_2; 2.
DR	PROSITE; PS50022; FA5B_C_3; 2.
DR	PROSITE; PS50060; MAM_2; 1.
KW	Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
KW	Alternative splicing.
FT	SIGNAL 1 20
FT	CHAIN 21 931
FT	DOMAIN 21 864
FT	TRANSEM 865 889
FT	DOMAIN 890 931
FT	DOMAIN 28 142
FT	DOMAIN 149 267
FT	DOMAIN 277 427
FT	DOMAIN 434 592
FT	DOMAIN 642 802
FT	DOMAIN 838 845
FT	DISULFID 28 55
FT	DISULFID 83 105
FT	DISULFID 149 175
FT	DISULFID 208 230
FT	DISULFID 277 427
FT	DISULFID 434 592
FT	CARBOHYD 152 152
FT	CARBOHYD 157 157
FT	CARBOHYD 629 629
FT	CARBOHYD 839 839
FT	VASAPLIC 809 813
PT	/ftid=vsp_004343.  POTENTIAL. NEUROFILIN-2. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). CUB 1. CUB 2. F5/8 TYPE C 1. F5/8 TYPE C 2. MAM. POLY-SER. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. N-LINKED (GLCNAC... ) (POTENTIAL). N-LINKED (GLCNAC... ) (POTENTIAL). N-LINKED (GLCNAC... ) (POTENTIAL). N-LINKED (GLCNAC... ) (POTENTIAL). Missing (in isoform A17). /ftid=vsp_004343.

FT VARSPLIC 809 830 Missing (in isoform A0).  
 FT FT /Frtid=VSP\_004344.  
 FT VARSPLIC 814 830 Missing (in isoform A5).  
 FT FT /Frtid=VSP\_004345.  
 FT VARSPLIC 810 931 EDFFVDLPETHGEGEYDEIDIDEYEGDMSSNSSTSGADP  
 FT CSYGEKMLYLTDILITLTIAMSISLGVLATCATCGLLYCT  
 FT CSYGSLASRSCCTLENNPFELYSOLKKHKVKINHOCCSEA  
 FT -> GLTPPGTEPTVDIVPVQPIPAWYWYMAAGAVLVLAS  
 FT VLVALVHYHFRFYAAKKTDSITYKTSHTNAPLAVEPLTLI  
 FT LTKLEGRGSHC (in isoform B0).  
 FT /Frtid=VSP\_004346.  
 FT VDIPETGEGEYDEIDIDEYEGDMSSNSSTSGADPPSCK  
 FT EKSMLVTLDILITIAMSISLGVLATCATCGLLYCTS  
 FT GLSRSCTTLENNFELIYDGLKKHKVKINHOCCSEA -->  
 FT GTLPPEGTPEPTVDIVPVQPIPAWYWYMAAGAVLVASVL  
 FT ALVLAHYHFRFYAAKKTDSITYKTSHTNAPLAVEPLTLI  
 FT KLEGRGSHC (in isoform B5).  
 FT /Frtid=VSP\_004347.  
 FT G-> I (IN REF. 1); AAC53380/AAC53381).  
 FT CONFLICT 786 786  
 FT SEQUENCE 931 AA; 104558 MM; 76FA4A4FP411D2F63 CRC64;

SQ

Query Match  
 Best Local Similarity 30.5%; Pred. No. 9.3e-06;  
 Matches 50; Conservative 18; Mismatches 71; Indels 25; Gaps 5;

Oy 1 MSLEGLLVTSALAGRRGTQAESNLSSKQPFSNKKGQGVDPQHRITTSTNGSIHS 60  
 Db 1 MDMPPLLTVFWFLA-----YESGHVRSQDDPCGGRPNSKDGYITS 42

Oy 61 PRPHPTPRNTVLWLVAVENVMIQLTFDERGLDEPDSDICKDYFEVE--EPEDGT 118  
 Db 43 PGYQDYPSHONCEMYIAPEPNOKILTANNPHEIKHD---CKDFIIIRGDSEASD 99

Oy 119 ILGRMGCGTGVPFKQISKGNQRIRFVSDEYFSPSEPFCIHYN 162  
 Db 100 LLGGHGCN-IAPTIISSGSVLVIKFSTD-YARGAGFSRYEI 141

RESULT 12

ID	TLD	BRARE	STANDARD;	PRT;	1022 AA.
AC		057460;			
DT	16-OCT-2001	(Rel. 40,	Created)		
DT	16-OCT-2001	(Rel. 40,	Last sequence update)		
DT	16-OCT-2001	(Rel. 40,	Last annotation update)		
DB	Dorsal-ventral patterning	tolloid protein precursor (EC 3.4.24.-)			
DB	(Mini fin protein).				
OS	TOLLIOID OR TLD OR MEN.				
OS	Brachydanto rerio (zebrafish) (danio rerio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OX	Cyprinidae; Danio.				
OX	NCBI_TaxId=7955;				
RN	[1]				
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.				
RC	TISSUE=Gastrula;				
RC	MEDLINE=98057457; PubMed=9395394;				
RA	Blader P., Rastegar S., Fischer N., Straehle U.;				
RA	"Cleavage of the BMP-4 antagonist chordin by zebrafish Tolloid.";				
RL	Science 278:1937-1940(1997).				
RN	[2]				
RP	FUNCTION, AND TISSUE SPECIFICITY.				
RX	MEDLINE=99307076; PubMed=10375503;				
RA	Connors S.A., Trout J., Ekker M., Mullins M.C.;				
RT	"The role of tolloids/minn fin in dorsoventral pattern formation of the				
RT	zebrafish embryo.";				
RL	Development 126:3119-3130(1999).				
CC	-1- FUNCTION: Required for patterning ventral tissues of the tail. May				
CC	increase bone morphogenetic protein (BMP) activity at the end of				
CC	gastrulation by proteolytic cleavage of chordin and release of BMP				
CC	from inactive complexes.				
CC	-1- TISSUE SPECIFICITY: During gastrulation, accumulates around the				
CC	closing blastopore with greater expression ventrally. At the				

CC		animal plate, expressed in the ectoderm flanking the anterior
CC		neural pole. At the 10-somite stage, expressed in the developing
CC		talband and cranial neural crest. At the 20-somite stage, also
CC	-1	expressed in the hematopoietic system.
CC	-1	SIMILARITY: Belongs to peptidase family M12A.
CC	-1	SIMILARITY: Contains 2 EGF-like domains.
CC	-1	SIMILARITY: Contains 5 CUB domains.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swais Institute of Bioinformatics and the EMBL outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC		or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC		-----
DR	EMBL; AF027596;	AACG0304.1; .-
DR	HSSP; P35555;	IEMN.
DR	MEROPS; M12.016;	-.
DR	ZFIN; ZDB-GENE-990415-265;	tolloid.
DR	InterPro; IPR000152;	Asx_hydroxy1_S.
DR	InterPro; IPR000859;	CUB.
DR	InterPro; IPR001881;	EGF_Ca.
DR	InterPro; IPR006209;	EGF_like.
DR	InterPro; IPR006025;	Pepf_M_Zn_BS.
DR	InterPro; IPR001506;	Peptidase_M12A.
DR	Pfam; PF01400;	Acatacin_1.
DR	Pfam; PF00431;	CUB; 5.
DR	Pfam; PF00008;	EGF; 2.
DR	PRINTS; PR00480;	ASTRACIN.
DR	SMART; SM00042;	CUB; 5.
DR	SMART; SM00179;	EGF_CA; 2.
DR	SMART; SM00235;	ZnMC; 1.
DR	PROSITE; PS00010;	ASX_HYDROXYL; 2.
DR	PROSITE; PS01180;	CUB; 5.
DR	PROSITE; PS00022;	EGF_1; FALSE_NEG.
DR	PROSITE; PS01186;	EGF_2; 2.
DR	PROSITE; PS50026;	EGF_3; 2.
DR	PROSITE; PS01187;	EGF_CA; 2.
DR	PROSITE; PS00142;	ZINC_PROTEASE; 1.
KW	Developmental protein;	Hydrolase; Protease; Metalloprotease; Zinc;
KW	Metal-binding; Calcium;	EGF-like domain; Repeat; Signal; Glycoprotein;
KW	Zymogen.	
KM	SIGNAL	1 32 POTENTIAL.
FT	SIGNAL	33 156 POTENTIAL.
FT	PROPEP	157 1022 DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN METALLOPROTEASE (BY SIMILARITY). CUB 1.
FT	CHAIN	157 1022
FT	DOMAIN	157 357 357 470 CUB 2.
FT	DOMAIN	358 470 CUB 2.
FT	DOMAIN	471 583 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	583 624 CUB 3.
FT	DOMAIN	627 739 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	739 779 CUB 4.
FT	DOMAIN	783 895 ZINC (CATALYTIC) (BY SIMILARITY).
FT	DOMAIN	896 1012 ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	249 249 ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT_SITE	250 250 ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	253 253 ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	259 259 ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISULFID	358 384 BY SIMILARITY.
FT	DISULFID	411 433 BY SIMILARITY.
FT	DISULFID	471 497 BY SIMILARITY.
FT	DISULFID	524 546 BY SIMILARITY.
FT	DISULFID	587 599 BY SIMILARITY.
FT	DISULFID	595 608 BY SIMILARITY.
FT	DISULFID	610 623 BY SIMILARITY.
FT	DISULFID	627 653 BY SIMILARITY.
FT	DISULFID	680 702 BY SIMILARITY.
FT	DISULFID	743 754 BY SIMILARITY.
FT	DISULFID	750 763 BY SIMILARITY.

FT	DISULFID	765	778	BY SIMILARITY.
FT	DISULFID	783	809	BY SIMILARITY.
FT	DISULFID	836	858	BY SIMILARITY.
FT	DISULFID	896	926	BY SIMILARITY.
FT	DISULFID	953	975	BY SIMILARITY.
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	368	368	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	399	399	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	635	635	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	1022 AA;	115536 MW;	A68CA1D0E41793F9 CRC64;
Query Match 8.6%: Score 159; DB 1; Length 1022;				
Best Local Similarity 39.8%; Pred. No. 1.4e-05;				
Matches 43; Conservative 19; Mismatches 38; Indels 8; Gaps 6				
QY	55	NGSIHSPFPHTYPTNTVLVRLVAVEENVMQLTFDERFGLEDPEDDICKYFVEVER-1133		
DB	635	NGITTPGMPKXEYPPNKKVCWQVVAFLQ-YRISMGF-EAFEELEG--NEVCCKDYVEVRG 630		
QY	114	-PSDGTILGRWCGSGTVPKQKISKGNQIRIRFVSDEYFPSEPGFCIHY 160		
DB	691	LSDSKHLGKYCGT-EVPEVITSGVNNMRIFKSDNTV-SKKGFKAHF 736		
RESULT 13				
NRPI_HUMAN				
ID	NRPI_HUMAN	STANDARD;	PRT;	923 AA.
AC	014786;	060461;		
DT	30-MAY-2000	(Rel. 39, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).			
GN	NRPI OR NRP OR VEGF165R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=97433084; PubMed=9288753;			
RA	He Z., Teesler-Lavigne M.;			
RT	"Neuropilin is a receptor for the axonal chemorepellent semaphorin			
RL	III.";			
RL	Cell 90:739-751(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39.			
RC	TISSUE=Breast;			
RX	MEDLINE=9618099; PubMed=9529250;			
RA	Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;			
RT	"Neuropilin-1 is expressed by endothelial and tumor cells as an			
RL	isoform-specific receptor for vascular endothelial growth factor.";			
RL	Cell 92:735-745(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31.			
RC	TISSUE=Prostatic adenocarcinoma;			
RX	MEDLINE=20183929; PubMed=1068880;			
RA	Gagnon M.L., Bieleberg D.R., Gechtman Z., Miao H.-Q., Takashima S.,			
RA	Soker S., Klagsbrun M.;			
RT	"Identification of a natural soluble neuropilin-1 that binds vascular			
RT	endothelial growth factor: In vivo expression and antitumor			
RT	activity.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).			
RN	[4]			
RP	CHARACTERIZATION.			
RX	MEDLINE=20309748; PubMed=10748121;			
RA	Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;			
RT	"Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid			
RT	form of vascular endothelial growth factor (VEGF) and of placenta			
RT	growth factor-2, but only neuropilin-2 functions as a receptor for			
RL	the 145-amino acid form of VEGF.";			
RL	J. Biol. Chem. 275:18040-18045(2000).			

CC -1- FUNCTION: The membrane-bound isoform 1 is a receptor involved in  
 CC the development of the cardiovascular system, in angiogenesis, in  
 CC the formation of certain neuronal circuits and in organogenesis  
 CC outside the nervous system. It mediates the chemorepulsive  
 CC activity of semaphorins. It binds to semaphorin 3A, the pLGF-2  
 CC isoform of PGF. The VEGF-165 isoform of VEGF and VEGF-B.  
 CC Coexpression with KDR results in increased VEGF-165 binding to KDR  
 CC as well as increased chemotaxis. It may regulate VEGF-induced  
 CC angiogenesis.  
 CC -1- FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to  
 CC inhibit its binding to cells. It may also induce apoptosis by  
 CC sequestering VEGF-165. May bind as well various members of the  
 CC semaphorin family. Its expression has an adverse effect on blood  
 CC vessel number and integrity.  
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein. Isoform 2 is  
 CC secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Membrane-bound;  
 CC IsoId=O14786-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Soluble, SNRP1;  
 CC IsoId=O14786-2; Sequence=VSP\_004339, VSP\_004340;  
 CC -1- TISSUE SPECIFICITY: The expression of isoforms 1 and 2 does not  
 CC seem to overlap. Isoform 1 is expressed by the blood vessels of  
 CC different tissues. In the developing embryo it is found  
 CC predominantly in the nervous system. In adult tissues, it is  
 CC highly expressed in heart and placenta; moderately in lung, liver,  
 CC skeletal muscle, kidney and pancreas; and low in adult brain.  
 CC Isoform 2 is found in liver hepatocytes, kidney distal and  
 CC proximal tubules.  
 CC -1- SIMILARITY: Belongs to the neuropilin family.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.  
 CC -1- SIMILARITY: Contains 1 MAM domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF018956; AAC51759.1; -;  
 CC EMBL; AF016050; AAC12921.1; -;  
 CC EMBL; AF145712; AAF44344.1; -;  
 CC PDB; 1KEX; 28-JAN-03  
 CC Genew; HGNC:8004; NRPL  
 CC MIM; 602069; -;  
 CC GO; GO:0005021; F:vascular endothelial growth factor receptor. .; TAS.  
 CC GO; GO:0007411; P:axon guidance; TAS.  
 CC GO; GO:0007267; P:cell-cell signaling; TAS.  
 CC GO; GO:0007397; P:histogenesis and organogenesis; TAS.  
 CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 CC GO; GO:0007165; P:signal transduction; TAS.  
 CC InterPro; IPR000859; CUB.  
 CC InterPro; IPR000421; FAS8\_C.  
 CC InterPro; IPR008979; Gal\_Bind\_Like.  
 CC InterPro; IPR000998; MAM\_domain.  
 CC Pfam; PF00431; CUB; 2.  
 CC Pfam; PF00754; F5\_F8\_Type\_C; 2.  
 CC Pfam; PF00629; MAM; 1.  
 CC PRINTS; PR00020; MAMDOMAIN.  
 CC SMART; SM00042; CUB; 2.  
 CC SMART; SM00231; FAS8C; 2.  
 CC SMART; SM00137; MAM; 1.  
 CC PROSITE; PS01180; CUB; 2.  
 CC PROSITE; PS01285; FAS8C\_1; 2.  
 CC PROSITE; PS01286; FAS8C\_2; 2.  
 CC PROSITE; PS50022; FAS8C\_3; 2.  
 CC PROSITE; PS00740; MAM\_1; 1.  
 CC PROSITE; PS50060; MAM\_2; 1.  
 CC Angiogenesis; Transmembrane; Glycoprotein; Neutrone; Signal; Repeat;

KW Receptor; Alternative splicing; 3D-structure.  
 FT SIGNAL 1 21  
 FT CHAIN 22 923  
 FT DOMAIN 22 856  
 FT TRANSMEM 857 879  
 FT DOMAIN 880 923  
 FT DOMAIN 27 141  
 FT DOMAIN 147 265  
 FT DOMAIN 275 424  
 FT DOMAIN 431 583  
 FT DOMAIN 645 811  
 FT DISULFID 27 54  
 FT DISULFID 82 104  
 FT DISULFID 147 173  
 FT DISULFID 206 228  
 FT DISULFID 275 424  
 FT DISULFID 431 583  
 FT CARBOHYD 150 150  
 FT CARBOHYD 261 261  
 FT CARBOHYD 300 300  
 FT CARBOHYD 522 522  
 FT CARBOHYD 842 842  
 FT VARSPPLIC 642 644  
 FT VARSPPLIC 645 923  
 FT CONFLICT 26 26  
 FT CONFLICT 749 749  
 FT CONFLICT 855 855  
 SQ SEQUENCE 923 AA; 103120 MW; ADEADCA4849E5D57 CRC64;  
 Query Match 8.5%; Score 158.5; DB 1; Length 923;  
 Best Local Similarity 35.7%; Pred. No. 1.4e-05;  
 Matches 41; Conservative 18; Mismatches 49; Indels 7; Gaps 4;  
 QY 50 IVYSTNGSIHSPPFTTTRNTVTVLRVLYAVEBNWITQTPBRRFLEDPEDICKYDV 109  
 DB 31 IKIESGYLTSGYPRSHYPSKCEWLIQAPPYGRIMNFPHPLEDRD--CKYDV 87  
 QY 110 EV--EESPDDGTLGRWCGSGTVPGKQISKGNQIRIRFVSDVDEVPSPGCIHYN 162  
 DB 88 EYFDGENENGRKRCCK-TAPPVSSGPFLFIKVS-D-YETHGAGFSIRYEI 140  
 RESULT 14  
 NRPL\_CHICK  
 ID NRPL\_CHICK STANDARD; PRT; 914 AA.  
 AC P79795;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 GN Neuropilin-1 precursor (AS protein).  
 OS NRPL OR NRP.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phaethidae; Phaethinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=White Leghorn; TISSUE=Embryonic brain;  
 RX MEDLINE=95324761; PubMed=7601310;  
 RA Takagi S., Kasuya Y., Shimizu M., Matsunura T., Tsuboi M., Kawakami A.,  
 RA Fujisawa H.;  
 RT "Expression of a cell adhesion molecule, neuropilin, in the  
 RT developing chick nervous system.";  
 RL Dev. Biol. 170:207-222 (1995).  
 CC -1- FUNCTION: Receptor involved in the development of the  
 CC cardiovascular system, in angiogenesis, in the formation of  
 CC certain neuronal circuits and in organogenesis outside the nervous  
 CC system. It mediates the chemorepulsive activity of semaphorins (By  
 CC similarity). Seems to have calcium-independent cell adhesion  
 CC properties.



CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Developing nervous system; optic tectum  
 CC (layers D and E of SGRS), amacrine cells of retina, neurites of  
 CC dorsal root ganglia. Also expressed in nonneuronal cells, e.g.  
 CC blood vessels in the entire embryo.  
 CC -1- SIMILARITY: Belongs to the neuropilin family.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.  
 CC -1- SIMILARITY: Contains 1 MAM domain.  
 CC -----  
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 CC -----  
 DR EMBL: D45416; BAA08256.1; -  
 DR HSSP: P12259; LC2T  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR000421; FAS8\_C.  
 DR InterPro: IPR008979; Gal Bind like.  
 DR InterPro: IPR000998; MAM\_domain.  
 DR Pfam: PF00431; CUB; 2.  
 DR Pfam: PF00754; F5\_P8\_type\_C; 2.  
 DR Pfam: PF00629; MAM; 1.  
 DR PRINTS: PR00020; MAMDOMAIN.  
 DR SMART: SM00042; CUB; 2.  
 DR SMART: SM00231; FAS8C; 2.  
 DR SMART: SM00137; MAM; 1.  
 DR PROSITE: PS01180; CUB; 2.  
 DR PROSITE: PS01285; FAS8C\_1; 2.  
 DR PROSITE: PS01286; FAS8C\_2; 2.  
 DR PROSITE: PS50022; FAS8C\_3; 2.  
 DR PROSITE: PS00740; MAM\_1; 1.  
 DR PROSITE: PS50060; MAM\_2; 1.  
 DR Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;  
 KM Receptor; Cell adhesion.  
 FT SIGNAL 1  
 FT CHAIN 18  
 FT DOMAIN 19 914  
 FT TRANSMEM 20 847  
 FT DOMAIN 848 870  
 FT DOMAIN 871 914  
 FT DOMAIN 25 139  
 FT DOMAIN 145 263  
 FT DOMAIN 429 581  
 FT DOMAIN 636 801  
 FT DISULFID 25 52  
 FT DISULFID 80 102  
 FT DISULFID 145 171  
 FT DISULFID 204 226  
 FT DISULFID 273 422  
 FT DISULFID 429 581  
 FT DISULFID 914 AA; 102480 MW; DD2EB6DF0CB68C CRC64;  
 SQ SEQUENCE 914 AA; 102480 MW; DD2EB6DF0CB68C CRC64;  
 Query Match 8.4%; Score 157; DB 1; Length 914;  
 Best Local Similarity 29.4%; Pred. No. 1.8e-05;  
 Matches 52; Conservative 27; Mismatches 68; Indels 30; Gaps 9;

RESULT 15  
 ID PCOI\_HUMAN STANDARD; PRT; 449 AA.  
 AC Q15113; Q14550;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I  
 DE procollagen COOH-terminal proteinase enhancer) (Type I procollagen C-  
 DE proteinase enhancer protein).  
 GN PCOLCE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RX MEDLINE=95014462; PubMed=7523404;  
 RA Takahara K., Kessler E., Biniatnikov L., Brusel M., Bddy R.L.,  
 RA Jantl-Salt S., Shows T.B., Greenspan D.S.;  
 RT "Type I procollagen COOH-terminal proteinase enhancer protein:  
 RT identification, primary structure, and chromosomal localization of the  
 RT cognate human gene (PCOLCE).";  
 RL J Biol. Chem. 269:26280-26285 (1994).  
 RN REVISTIONS TO 56; 154 AND 373.  
 RA Kessler E.;  
 RL Unpublished observations (FEB-2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Hirahara I., Syoutfuda K., Harada K., Tomita M., Urakami K., Terai H.,  
 RA Morisaki N., Saito Y.;  
 RT "Smooch muscle cell derived procollagen C-protease enhancer protein";  
 RL Cell Struct. Funct. 21:662-662 (1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99018118; PubMed=9799793;  
 RA Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,  
 RA Teul L.-C., Rosenthal A.;  
 RT "Large-scale sequencing of two regions in human chromosome 7q22:  
 RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci  
 RT reveals 17 genes";  
 RL Genome Res. 8:1060-1073 (1998).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=99134301; PubMed=9933570;  
 RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;  
 RT "Structural organization and expression patterns of the human and  
 RT mouse genes for the type I procollagen COOH-terminal proteinase  
 RT enhancer protein";  
 RL Genomics 55:229-234 (1999).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,  
 RA Rata S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huily S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.  
 RX MEDLINE=20092917; PubMed=10625689;  
 RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,  
 RA Banda M.J.;  
 RT "post-translational proteolytic processing of procollagen C-terminal  
 proteinase enhancer releases a metalloproteinase inhibitor.";  
 RL J. Biol. Chem. 275:1384-1390(2000).  
 CC -|- FUNCTION: Binds to the COOH-terminal propeptide of type I  
 CC procollagen and enhances procollagen C-proteinase activity.  
 CC -|- FUNCTION: C-terminal processed part of PCPE (CT-PCPE) may have an  
 CC metalloproteinase inhibitory activity.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- PTM: C-terminally processed at multiple positions.  
 CC -|- SIMILARITY: Contains 2 CUB domains.  
 CC -|- SIMILARITY: Contains 1 NTR domain.  
 CC -----  
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 CC -----  
 DR EMBL; L33799; AAA61949.1; ALT\_SEQ.  
 DR EMBL; AB008549; BAA23281.1; -;  
 DR EMBL; AF053356; AAC78800.1; -;  
 DR EMBL; AF083655; AAD16041.1; -;  
 DR EMBL; BC000574; AA00574.1; -;  
 DR EMBL; BC033205; AA033205.1; -;  
 DR GeneW; HGNC:8738; PCOLCE.  
 DR MIM; 600270; -;  
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.  
 DR GO; GO:0007275; P:development; TAS.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR001134; Netrin\_C.  
 DR Pfam; PF00451; CUB; 2.  
 DR Pfam; PF01759; NTR; 1.  
 DR SMART; SM00643; C345C; 1.  
 DR SMART; SM00042; CUB; 2.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS50189; NTR; 1.  
 DR GlycoProtein; Repeat; Signal.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 449 PROCOLLAGEN C-PROTEINASE ENHANCER  
 FT PROTEIN.  
 FT DOMAIN 37 149 CUB 1.  
 FT DOMAIN 159 273 CUB 2.  
 FT DOMAIN 318 437 NTR.  
 FT SITE 287 288 CLEAVAGE.  
 FT SITE 288 289 CLEAVAGE.  
 FT SITE 293 294 CLEAVAGE.  
 FT SITE 299 300 CLEAVAGE.  
 FT SITE 303 304 CLEAVAGE.  
 FT CARBOHYD 29 29 N-LINKED (GLCNAC.. ) (POTENTIAL).  
 FT CARBOHYD 431 431 N-LINKED (GLCNAC.. ) (POTENTIAL).  
 SQ SEQUENCE 449 AA; 47972 MW; 3D86430158648796 CRC64;

Query Match 8.3%; Score 154; DB 1; Length 449;

Best Local Similarity 33.8%; Pred. No. 1.3e-05;  
 Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;

QY 56 GSIIHSPFPH-T-YPRNTVLVWRLVAVEENWVQLTFDERGLEDPEDDICKYDFVEV---111  
 Db 168 GTLTTPWPSDYPFGISGSMHIIAPPDV-IALTF-EKFDLE--PTYICRYSVSVENG 223

QY 112 EEPDGTILGRWCGSGTVPQKISKNGIRIRFVSDVEYFSPGFCIHNYVMPQT---168  
 Db 224 AVSDDRRLRGKFCGD-AVPGSISSEGNELVGFVSDLSVTAD-GFASAYK-TLPGTAXE 280  
 QY 169 -----EAVSPGV-LPPSALP 182  
 Db 281 GGGPGPRGTGTEPKVKLPPKSP 302

Search completed: May 27, 2004, 15:45:16  
 Job time : 12.5 secs



Best Local Similarity 100.0%; Pred. No. 3.1e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLVTSALAGRGTOAESNLSKFOSSNKQNGVDPQHERITITVSTNGSIHS 60  
DB 1 MSFGLLVTSALAGRGTOAESNLSKFOSSNKQNGVDPQHERITITVSTNGSIHS 60  
QY 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120  
DB 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120  
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSPGCIHYNIMVMPQTEAVSPSVLPSPA 180  
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSPGCIHYNIMVMPQTEAVSPSVLPSPA 180  
QY 181 LPDLNNATITAFSTLEDLIRYLEPERMQLDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240  
DB 181 LPDLNNATITAFSTLEDLIRYLEPERMQLDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240  
QY 241 LEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
DB 241 LEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
QY 301 VTKKHEVQLRPKTVGRGLHKSITDVALHHEBCDCVCRGSGTGG 345  
DB 301 VTKKHEVQLRPKTVGRGLHKSITDVALHHEBCDCVCRGSGTGG 345

## RESULT 2

Q9UL22 PRELIMINARY; PRT; 345 AA.

AC Q9UL22; PRELIMINARY; PRT; 345 AA.  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Secretory growth factor-like protein PALLONEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).  
GN HSCDGF OR PDGFC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RA Tsai Y.-J., Lee R.K.-K., Lin S.-P.;  
RT "Pallonein, a novel growth factor like gene identified in human uterus." (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20317014; Pubmed=10858496;  
RA Hamada T., Ue-Tai K., Miyata Y.;  
RT "A novel gene derived from developing spinal cords, SCDF, is a unique member of the PDGF/VEGF family.";  
RL FEBS Lett. 475:97-102(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21347863; Pubmed=11297552;  
RA Gilbertson D.G., Duff M.B., West J.W., Kelly J.D., Sheppard P.O., Hofstad P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;  
RT "Platelet-derived growth factor C (PDGF-C), a Novel Growth Factor That binds to PDGF alpha and beta Receptor.";  
RL J. Biol. Chem. 276:27406-27414(2001).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AF091434; AAF00049.1; -;  
DR EMBL; AB033831; BAB03266.1; -;  
DR EMBL; AF260738; AAK51637.1; -;  
DR GO; GO:0005576; C:extracellular; NMS.  
DR GO; GO:0008083; F:growth factor activity; TAS.  
DR GO; GO:0007417; P:central nervous system development; TAS.

DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF 2; 1.  
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 99.6%; Score 1851; DB 4; Length 345;  
Best Local Similarity 99.4%; Pred. No. 1.5e-172;  
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLVTSALAGRGTOAESNLSKFOSSNKQNGVDPQHERITITVSTNGSIHS 60  
DB 1 MSFGLLVTSALAGRGTOAESNLSKFOSSNKQNGVDPQHERITITVSTNGSIHS 60  
QY 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120  
DB 61 PREPHTYPRNTVLMRLVAEENVMQLTFDERFGLEDEDDICKYDFVEEPPSDGTL 120  
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSPGCIHYNIMVMPQTEAVSPSVLPSPA 180  
DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDDEYFPSPGCIHYNIMVMPQTEAVSPSVLPSPA 180  
QY 181 LPDLNNATITAFSTLEDLIRYLEPERMQLDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240  
DB 181 LPDLNNATITAFSTLEDLIRYLEPERMQLDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240  
QY 241 LEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
DB 241 LEEVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
QY 301 VTKKHEVQLRPKTVGRGLHKSITDVALHHEBCDCVCRGSGTGG 345  
DB 301 VTKKHEVQLRPKTVGRGLHKSITDVALHHEBCDCVCRGSGTGG 345

## RESULT 3

Q9QY71 PRELIMINARY; PRT; 345 AA.

AC Q9QY71; PRELIMINARY; PRT; 345 AA.  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Pallonein (Platelet-derived growth factor C).  
GN Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;  
RT "cDNA cloning of fallotein from mouse ovary.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Gilbertson D., West J., O'Hara P.J.;  
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;  
RX MEDLINE=22354683; Pubmed=12466851;  
RA The FANTOM Consortium;  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of

RT 60, 770 full-length cDNA." ;  
RL Nature 420:563-573(2002).  
CC -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AF117608; AAF22516.1; -;  
DR EMBL; AF266467; AAK58566.1; -;  
DR EMBL; AF033734; BAC28455.1; -;  
DR EMBL; AK042767; BAC31358.1; -;  
DR EMBL; AK052947; BAC35216.1; -;  
DR MGD; MGI:1859631; Pdgc.  
DR GO; GO:0005576; C:extracellular; IDA.  
DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. . .; IDA.  
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.  
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SMO0042; CUB; 1.  
DR SMART; SMO0141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF\_2; 1.  
DR PROSITE; PS50278; PDGF\_2; 1.  
SQ SEQUENCE 345 AA; 38741 MM; 3A58A1F701B84EA2 CRC64;  
Query Match 89.6%; Score 1664; DB 11; Length 345;  
Best Local Similarity 86.7%; Pred. No. 3e-154;  
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MSLFGLLVTSALAGORRGTQAEENLSKFPQSSNKEQNGVQDPQHERITVSTNGSIHS 60  
DB 1 MLLGLLLITLSALAGORTGRAESNLSKLTQSSDKQNGVQDPQHERVITISNGSIHS 60  
QY 61 PRPHPTVPRNTVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSDGTL 120  
DB 61 PKPHTVPRNVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSDGSL 120  
QY 121 GRMGSGTVPGKQSKGNQIRIRFVSDSEYFSEBGFCHYNYVMPQTEAVSPVLPSSA 180  
DB 121 GRMGSGTVPGKQSKGNHIRIRFVSDSEYFSEBGFCHYNYVMPQTEAVSPVLPSS 180  
QY 181 LPLDLNNATAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVDNL 240  
DB 181 LSLDLNNATVAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVDNL 240  
QY 241 LEEVRLYSCTPRNFSVSIRESLRTDTTFPFGCLLVRCGNCACCLHNCNCCQVPSK 300  
DB 241 LKEEVKLYSCTPRNFSVSIRESLRTDTTFPFGCLLVRCGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKYHEVLQLRPKTVGKGLKSLTDVALLEHHEBCDCVCRGNAGG 345  
DB 301 VTKKYHEVLQLRPKTVGKGLKSLTDVALLEHHEBCDCVCRGNAGG 345  
RESULT 4  
Q8C119 PRELIMINARY; PRT; 345 AA.  
ID Q8C119  
AC Q8C119  
DT 01-MAR-2003 (TREMblrel. 23, Created)  
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
DE Platelet-derived growth factor, C polypeptide.  
GN PDGFC.  
OS Mus musculus (Mouse).  
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CZECH II;  
RA Strauberg R.;  
RL Submitted (Sep-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC037696; AAH37696.1; -;  
DR MGD; MGI:1859631; Pdgc.  
DR GO; GO:0005576; C:extracellular; IDA.

DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. . .; IDA.  
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.  
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SMO0042; CUB; 1.  
DR SMART; SMO0141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF\_2; 1.  
SQ SEQUENCE 345 AA; 38741 MM; 9A58A05C6C0B9614 CRC64;  
Query Match 89.5%; Score 1662; DB 11; Length 345;  
Best Local Similarity 86.4%; Pred. No. 4.8e-154;  
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MSLFGLLVTSALAGORRGTQAEENLSKFPQSSNKEQNGVQDPQHERITVSTNGSIHS 60  
DB 1 MLLGLLLITLSALAGORTGRAESNLSKLTQSSDKQNGVQDPQHERVITISNGSIHS 60  
QY 61 PRPHPTVPRNTVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSDGTL 120  
DB 61 PKPHTVPRNVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSDGSL 120  
QY 121 GRMGSGTVPGKQSKGNQIRIRFVSDSEYFSEBGFCHYNYVMPQTEAVSPVLPSSA 180  
DB 121 GRMGSGTVPGKQSKGNHIRIRFVSDSEYFSEBGFCHYNYVMPQTEAVSPVLPSS 180  
QY 181 LPLDLNNATAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVDNL 240  
DB 181 LSLDLNNATVAFSTLEDLIRYLEPERWQDLIEDLYRPTWQLGKAFVGRKSRVDNL 240  
QY 241 LEEVRLYSCTPRNFSVSIRESLRTDTTFPFGCLLVRCGNCACCLHNCNCCQVPSK 300  
DB 241 LKEEVKLYSCTPRNFSVSIRESLRTDTTFPFGCLLVRCGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKYHEVLQLRPKTVGKGLKSLTDVALLEHHEBCDCVCRGNAGG 345  
DB 301 VTKKYHEVLQLRPKTVGKGLKSLTDVALLEHHEBCDCVCRGNAGG 345  
RESULT 5  
Q9EOX6 PRELIMINARY; PRT; 345 AA.  
ID Q9EOX6  
AC Q9EOX6  
DT 01-MAR-2001 (TREMblrel. 16, Created)  
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
DE Spinal cord-derived growth factor.  
GN RSCDGF.  
OS Rattus norvegicus (Rat).  
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Missar; TISSUE=Kidney;  
RC MEDLINE=21092670; PubMed=11162582;  
RA Hamada T., Ue-Tel K., Imaki J., Miyata Y.;  
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to SCDF/BDGF-C/falotin." ;  
RT SCDF/BDGF-C/falotin." ;  
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).  
CC -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AB033830; BAB19969.1; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008083; F:growth factor activity; IEA.  
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SMO0042; CUB; 1.

DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF; 2; 1.  
SQ SEQUENCE 345 AA; 38734 MW; F296DA6B9B765D10 CRC64;

Query Match 88.6%; Score 1646; DB 11; Length 345;  
Best Local Similarity 85.5%; Pred. No. 1.8e-152;  
Matches 295; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

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QY 1 MSIFGLLVTSAAGRGRTQAESENLSKRFQSSNKONGVODPOHERITITVSTNGSIHS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MLLIGLLLTSAAGRTGTRAESENLSKQLQSSDKQNGVODPRERVVTISGNSIHS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PREPHTYPRNTVLVWRLVAEENWVIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PKFPHYTPRNTVLVWRLVAEENWRIQLTFDERFGLEDEDDICKYDFVEVEPSDGSVL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GRWCGSGTVPKQKISGKNQIRIRFVSDEYFPSPGFCIHNYIMVPOFTEAVSPVLPSPA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GRWCGSGTVPKQKISGKNHIRIRFVSDEYFPSPGFCIHYSIIMPQVETTTSPSVLPSPA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LPLDLNNATAPSTLEDLIRYLEPBRWOLDLDRPTWQLGKAFFGKRGKRVVDLNL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LSLDLNNATAPSTLELIRYLEPBRWQIDLSLYKPTWPLGKAFLYGKSKKAVNLNL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 LTRVRLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LKEEVKLYSGTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 VTKKHYEVQLRPTKTVGRGLHKSITDVALHHEBECDCVCRGSTGG 345
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VTKKHYEVQLRPTKTVGRGLHKSITDVALHHEBECDCVCRGSTGG 345
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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## RESULT 6

Q9JHV8 PRELIMINARY; PRT; 345 AA.

ID Q9JHV8  
AC Q9JHV8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Platelet-derived growth factor C.  
GN PDGFC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Swiss-Webster/NIH;  
RX MEDLINE=20417814; PubMed=10960785;  
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;  
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during  
RT organogenesis.";  
RT Mech. Dev. 96:209-213(2000).  
RL -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
CC EMBL; AF286725; AAF91483.1; -.  
DR MGD; MG1:1859631; PdGfc.  
DR GO; GO:0005576; C:extracellular; IDA.  
DR GO; GO:0005161; F:platelet-derived growth factor receptor bin.; IDA.  
DR GO; GO:0008284; F:positive regulation of cell proliferation; IDA.  
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin.; IDA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; PDGF; 1.  
DR PROSITE; PS50278; PDGF; 2; 1.  
SQ SEQUENCE 345 AA; 38886 MW; FA1486BEDD362F8 CRC64;

Query Match 88.0%; Score 1635; DB 11; Length 345;  
Best Local Similarity 85.5%; Pred. No. 2.1e-151;

Matches 295; Conservative 28; Mismatches 22; Indels 0; Gaps 0;

```

QY 1 MSIFGLLVTSAAGRGRTQAESENLSKRFQSSNKONGVODPOHERITITVSTNGSIHS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MLLIGLLLTSAAGRTGTRAESENLSKQLQSSDKQNGVODPRERVVTISGNSIHS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PREPHTYPRNTVLVWRLVAEENWVIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PKFPHYTPRNTVLVWRLVAEENWRIQLTFDERFGLEDEDDICKYDFVEVEPSDGSVL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GRWCGSGTVPKQKISGKNQIRIRFVSDEYFPSPGFCIHNYIMVPOFTEAVSPVLPSPA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GRWCGSGTVPKQKISGKNHIRIRFVSDEYFPSPGFCIHYSIIMPQVETTTSPSVLPSPA 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LPLDLNNATAPSTLEDLIRYLEPBRWOLDLDRPTWQLGKAFFGKRGKRVVDLNL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LSLDLNNATAPSTLELIRYLEPBRWQIDLSLYKPTWPLGKAFLYGKSKKAVNLNL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 LTRVRLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LKEEVKLYSGTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 VTKKHYEVQLRPTKTVGRGLHKSITDVALHHEBECDCVCRGSTGG 345
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VTKKHYEVQLRPTKTVGRGLHKSITDVALHHEBECDCVCRGSTGG 345
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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## RESULT 7

Q91946 PRELIMINARY; PRT; 345 AA.

ID Q91946  
AC Q91946;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Spinal cord-derived growth factor.  
GN SCDGF.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OX Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=White Leghorn; TISSUE=Spinal cord;  
RX MEDLINE=20317014; PubMed=10858496;  
RA Hamada T., Ui-Rei K., Miyata Y.;  
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique  
RT member of the PDGF/VEGF family.";  
RT FEBS Lett. 475:97-102(2000).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AB033829; BAB03265.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008083; F:growth factor activity; IEA.  
DR GO; GO:0008151; F:cell growth and/or maintenance; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR SMART; SM00041; PDGF; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; PDGF; 1.  
DR PROSITE; PS50278; PDGF; 2; 1.  
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA92BF5128C CRC64;

Query Match 86.9%; Score 1614; DB 13; Length 345;  
Best Local Similarity 83.8%; Pred. No. 2.4e-149;  
Matches 289; Conservative 31; Mismatches 25; Indels 0; Gaps 0;

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QY 1 MSIFGLLVTSAAGRGRTQAESENLSKRFQSSNKONGVODPOHERITITVSTNGSIHS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MLLIGLLLTSAAGRTGTRAESENLSKQLQSSDKQNGVODPRERVVTISGNSIHS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PREPHTYPRNTVLVWRLVAEENWVIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 61 PKPHTYRNTVTLVWRLVAVDENWVLTQTFDERFGLDEDPEDICKYDFVEVEBPSDGLVTL 120  
Qy 121 GRMGSGVTPGKQISKGNQIRIRFVSDYFSPSEPCFCHNINWVQFPAVSPVLPSPA 180  
Db 121 GRMGSSSVPSRQISKGNQIRIRFVSDYFSPSEPCFCHNINWVQFPAVSPVLPSPA 180  
Qy 181 LPLDLNNAITAFSTLEDLIRYLEPERWQLEDLIRPTWOLGAFVGRKSRVVDNL 240  
Db 181 LPLDLNNAITAFSTLEDLIRYLEPERWQLEDLIRPTWOLGAFVGRKSRVVDNL 240  
Qy 241 LTBEEVRLVSCTPRNFVSISREELKRTDTIFMPGCLVRCGNCACCLHNCNCCVPSK 300  
Db 241 LKEEVRVLSCTPRNFVSISREELKRTDTIFMPGCLVRCGNCACCLHNCNCCVPSK 300  
Qy 301 VTKKYHEVLRPKTGVGKSLTDVLAHEHBCDCVCRSGTG 345  
Db 301 VTKKYHEVLRPKTGVGKSLTDVLAHEHBCDCVCRSGTG 345

## RESULT 8

09K429 PRELIMINARY; PRT; 258 AA.  
ID 09K429  
AC 09K429;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Platelet-derived growth factor C (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Skin;  
RA Brown S.A., Goberly D.M., Rohrich R.R., Chao J.J.;  
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound Healing."  
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AF508348; AAM47265.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008083; F:growth factor activity; IEA.  
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR00072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR SMART; SM00042; CUB; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 258  
SQ SEQUENCE 258 AA; 29255 MM; 88625B989CC3F8B CRC64;  
Query Match 67.8%; Score 1260; DB 11; Length 258;  
Best Local Similarity 85.6%; Pred. No. 7.3e-115;  
Matches 220; Conservative 25; Mismatches 12; Indels 0; Gaps 0;  
Qy 42 QDPQHERITVSTNGSIHSPRPHTYRNTVTLVWRLVAVDENWVLTQTFDERFGLDEDP 101  
Db 1 QDPHERVVTISGNGSIHSPKPHYRNTVTLVWRLVAVDENWVLTQTFDERFGLDEDP 60  
Qy 102 DICXYDPVEVEBPSDGLVGRMGSGVTPGKQISKGNQIRIRFVSDYFSPSEPCFCHN 161  
Db 61 DLCKYDFVEVEBPSDGLVGRMGSGVTPGKQISKGNQIRIRFVSDYFSPSEPCFCHN 120  
Qy 162 IVMQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERWQLEDLIRPTWQ 221  
Db 121 IIMQVETTSVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERWQLEDLIRPTW 180  
Qy 222 LLGKAFVGRKSRVVDNLTLTBEEVRLVSCTPRNFVSISREELKRTDTIFMPGCLVRCG 281  
Db 181 LLGKAFVGRKSRVVDNLTLTBEEVRLVSCTPRNFVSISREELKRTDTIFMPGCLVRCG 240

Qy 282 GNCACCLHNCNCCVCP 298  
Db 241 GNCACCLHNCNCCVCP 257

## RESULT 9

09GZP0 PRELIMINARY; PRT; 370 AA.  
ID 09GZP0  
AC 09GZP0;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE SPINAL CORD-derived growth factor-B (MSP036) (IRS-expressed growth factor long form) (Platelet-derived growth factor D).  
GN HSCDGF-B OR IEGF OR PDGFD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Hamada T., Yi-Tei K., Imaki J., Miyata Y.;  
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF/PDGF-C/fallotrin."  
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Aorta;  
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,  
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,  
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,  
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;  
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=iris;  
RA Wistow G.;  
RL "iris-expressed Growth Factor (IRGF).";  
RT Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC PubMed=1133181;  
RA Bergsten E., Untela M., Li X., Pietras K., Ostman A., Heldin C.H.,  
RA Alltato K., Eriksson U.;  
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-receptor."  
RL Nat. Cell Biol. 3:512-516(2001).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=21231380; PubMed=11331882;  
RA Larochele W.J., Jeffers M., McDonald W.F., Chillaakuru R.A., Vernet C.,  
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,  
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,  
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;  
RT "PDGF D, A Novel Protease-Activated Growth Factor."  
RL Nat. Cell Biol. 3:517-521(2001).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AB033832; BAB18903.1; -.  
DR EMBL; AF113216; AAC39287.1; -.  
DR EMBL; AY027517; AAK20081.1; -.  
DR EMBL; AF36376; AAK56136.1; -.  
DR EMBL; AF35584; AAK38840.1; -.  
DR PIR; JC7591; JC7591.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008083; F:growth factor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR00072; PD\_growth\_factor.  
DR InterPro; IPR000531; TonB\_box.  
DR Pfam; PF00431; CUB; 1.





RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nomura R., Ono M.,  
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai K.,  
 RA Sano H., Saeki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 RA Sobue Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.; to the EMBL/GenBank/DBJ databases.  
 RU Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Mech. Enzymol. 303:19-44 (1999).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kitanaka T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaibiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matakaki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL: AF335583; AK38839.1; -;  
 DR EMBL: AK003359; BAB2735.2; -;  
 DR MGI: 1919035; Pdgf.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0008083; F:growth factor activity; IEA.  
 DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR000721; PD\_growth\_factor.  
 DR Pfam: PF00431; CUB; 1.  
 DR SMART: SM0042; CUB; 1.  
 DR SMART: SM00141; PDGF; 1.  
 DR PROSITE: PS01180; CUB; 1.  
 DR PROSITE: PS50278; PDGF\_2; 1.  
 DR PROSITE: PS50278; PDGF\_2; 1.  
 SO SEQUENCE 370 AA; 42809 MW; 958084CF6813BFB6 CRC64;

Query Match 39.7%; Score 737.5; DB 11; Length 370;  
 Best Local Similarity 44.0%; Pred. No. 1.7e-63;

Matches 153; Conservative 59; Mismatches 103; Indels 33; Gaps 9;  
 QY 16 QKRTQAESLSKFFQSSKKEQNVOD -PQHERITVSTNGSHSRPFRPTVTV 74  
 Db 26 QRSIKALRNANR-----RDESNHLDLYQREBNIOVTNGHQSPFPNSPRNLLT 80  
 QY 75 WRLVAVENWIGLTPDERGLDEDDICKYQFVEVEESDGT--ILGRMGSGTVPGK 132  
 Db 81 WMLRS-DEKTRIQSPFHQGLBEAENDICRDFVEVEEVSSTTVYGRMGKHEIPPR 139  
 QY 133 QISKNGQIRIRFVSDVEPSPGFCIHNYIMQFTAV-----SPS 174  
 Db 140 ITRKTNQIKITFMSDVFVAKPGKITYSPVEDPQPEAASETWSTSSFSGVSYHSPS 199  
 QY 175 VLPPSALPLDNLNNAITAEFTEDLRYLEPERKQOLDLNYPTWOLGKAFVPGKR 234  
 Db 200 ITDPT-LTADALPKTVAEPFTVEDLHGFNVSMODLENYLDTPIYRRSY-HDKSK 257  
 QY 235 VVDNLTLTEEVRLYSCPTPRNFVSIRBELKRTDTIPWPGCLVYRCGACACCLHNCNC 294  
 Db 258 -VDLDRINDVYKSCPTPRNHSVNLRELLKLTNAVFPRCLLYQRCGACCGCTVMKSC 316  
 QY 295 QCVPSKVTXKYHEVTLQLRP--KTGYRGLHKSJLTDVALHHEBCDVCV 339  
 Db 317 TCSSGKTVKXKXHEVTLKPEPGHFKRGRKAKMVALVDIGDHRRCDCIC 364  
 RESULT 12  
 Q9E0T1 PRELIMINARY; PRT; 370 AA.  
 AC Q9E0T1;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Spinal-cord derived growth factor-B.  
 GN RSCDGF-B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21092670; PubMed=11162582;  
 RA Hamada T., Ue-Tai K., Imaki J., Miyata Y.;  
 RT "Molecular cloning of SCDF-B, a Novel Growth Factor Homologous to  
 RT SCDF/PDGF-C/fallotcin.";  
 RL Biochem. Biophys. Res. Commun. 280:733-737 (2001).  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL: AB052170; BAB18920.1; -;  
 DR PIR: JC7592; JC7592.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0008083; F:growth factor activity; IEA.  
 DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR000721; PD\_growth\_factor.  
 DR Pfam: PF00431; CUB; 1.  
 DR SMART: SM0042; CUB; 1.  
 DR SMART: SM00141; PDGF; 1.  
 DR PROSITE: PS01180; CUB; 1.  
 DR PROSITE: PS50278; PDGF\_2; 1.  
 DR PROSITE: PS50278; PDGF\_2; 1.  
 SO SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;

Query Match 39.6%; Score 736; DB 11; Length 370;  
 Best Local Similarity 45.6%; Pred. No. 2.4e-63;  
 Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;  
 QY 37 EQNGVOD-PQHERITVSTNGSHSRPFRPTVTVWRLVAVENWIGLTPDERFG 95  
 Db 42 ESNHLDLYRDRNIRITGTGHVQSPFPNSPRNLLTWRHS-DEKTRIQALPDHFG 100  
 QY 96 LEDPEDDICKYQFVEVEESDGT--ILGRMGSGTVPGKQISKNGQIRIRFVSDVEPSP 153  
 Db 101 LBEAENDICRDFVEVEEVSSTTVYGRMGKHEIPRITRNTQIKITFQSDDYVAK 160

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QY 154 PGFCIHNYIV---MPOFTEAV-----SPSVLPSPALPLDILNNATAFST 195
DB 161 PGFKIYVSFVEDPOPEAASEINNESVTSFSGVSYHSPWM-DSTLADALDRAIAEFDT 219
QY 196 LEBLIRLEPERQQLDEDLYRPTWOLGKAFFGKRSRVVDNLTEERLYLSCPTPRNF 255
DB 220 VEDLLKTFNPASQODDLEMLYMDTPRKYGRSY-HERKSK-VDLDRINDVDYKRYSCPTPRNF 277
QY 256 SVSIREELKRTDITFMFGCLLVKRCGNCACCLHNCGCCVDPSTKYKHYEVLQLRP-- 313
DB 278 SVULREELKLTNAVFFRCCLLVORCGNCCGTLNWKSCCTCSSGKYKHYEVLKEPFGH 337
QY 314 -KTGVAGLKSITVDVALLEHNECDVCV 339
DB 338 FKRGRKAKNMALVDIQLDHERCDIC 364

RESULT 13
Q8K2L3 PRELIMINARY; PRT; 261 AA.
AC 08K2L3;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to platelet-derived growth factor, D polypeptide.
GN PDGFD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; BC030896; AA030896.1; -.
DR MGD; MGI:1919035; PdGfd.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 261 AA; 30228 MW; 2EEC3F6373A52D09 CRC64;

Query Match 23.4%; Score 435.5; DB 11; Length 261;
Best Local Similarity 39.8%; Pred. No. 3.9e-34;
Matches 97; Conservative 45; Mismatches 73; Indels 29; Gaps 7;
QY 16 QRRGTQAEBSLSSKQFSSNKEQNGVOD-PQHERITVSTNGSIHSPRPPTTYPRNTVLY 74
DB 26 QRRSIALRNVANLR-----RDESNHLTDLQREENIQVTSNGHVQSPRPFNSTYPRNLLLT 80
QY 75 WRLVAEENVMWLTDFDERFGLDEPDIDCKYDFVEEPEPSDGT--ILGWCQSGVTPCK 132
DB 81 WMLRS-QEKTRIDLSDDHQGLGEAENDICRIDFVEEVESESTYVGRMGCHKEIPRR 139
QY 133 QISKGNQIRIRFVSDYFPEBEPFCIHNYIVMPQFTEAV-----SPS 174
DB 140 ITRTQIKITFKSDDYFVAKPGFKIYVSFVEDSQPEAASETWESVTSFSGVSYHSPS 199
QY 175 VLPSPALPLDILNNATAFSTLEDLIRYLEPERQQLDEDLYRPTWOLGKAFFGKRSR 234
DB 200 ITDPT-LTADALDKTVAEPDVEDLKHFNPSVQDLEMLYLDTPHYRGRSY-HDRKSK 257
QY 235 VVDL 238
DB 258 GIEV 261

RESULT 14
Q8QFX6 PRELIMINARY; PRT; 923 AA.
AC 08QFX6;

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DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Neuropilin-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OX Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RA SEQUENCE FROM N.A.
RA Lee P., Goshl K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
RT "Neuropilin-1 is required for normal vascular development and is a
RT mediator of VEGF-dependent angiogenesis in zebrafish."
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
DR EMBL; AY064213; AAL40862.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR008979; Gal Bind like.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_Type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS8C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FAS8C_1; 1.
DR PROSITE; PS01286; FAS8C_2; 2.
DR PROSITE; PS00022; FAS8C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
DR GlycoProtein; Receptor; Transmembrane.
SQ SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;

Query Match 10.3%; Score 190.5; DB 13; Length 923;
Best Local Similarity 27.6%; Pred. No. 2.1e-09;
Matches 66; Conservative 29; Mismatches 95; Indels 49; Gaps 8;
QY 5 GLLVTSALAGRRGTQAEBSLSSKQFSSNKEQNGVODPQHERITVSTNGSIHSPRP 64
DB 12 GFLVYSALKNDKCGDN-----IRTSANYLTSPGYP 43
QY 65 HTYPRNTVWRLVAEENVMWLTDFDERFGLDEPDIDCKYDFVEEPEPSD--GTILGR 122
DB 44 VHYPSQKCIWITAPGPNQRLINPNPHFLEDR--CKDYVEVRDQVDENGQLVCK 100
QY 123 WCGSGTVPKQISKGNQIRIRFVSDYFPEBEPFCIHNYIVMPQFTEAVSPSVL 176
DB 101 YCGK-IAPSPVVSQGNQLFKFVSD-YETHGAGFSIRYEIPFTGPECSNFTS--SSGVI 156
QY 177 PPSALPLDILNNATAFSTLEDLIRYLEPERQQLDEDLYRPTWOLGKAFFGKRSR 235
DB 157 KSPGPEPKYPNMLDCTFMIFAPKMSIYLFESFELPDTQ-----PAGVCRYDRL 209

RESULT 15
Q8AXP1 PRELIMINARY; PRT; 923 AA.
AC 08AXP1;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Neuropilin-1.
GN NP-1.

```

OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shoji W., Tawarayama H.;  
RT "The cloning and expression of neuropilin-1";  
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AB088776; BAC53657.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000421; PA58\_C.  
DR InterPro; IPR008979; Gal\_Bind\_like.  
DR InterPro; IPR000998; MAM\_domain.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00754; F5\_F8\_type\_C; 2.  
DR Pfam; PF00629; MAM; 1.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00231; PA58C; 2.  
DR SMART; SM00137; MAM; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01285; PA58C\_1; 1.  
DR PROSITE; PS01286; PA58C\_2; 2.  
DR PROSITE; PS50022; PA58C\_3; 2.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS50060; MAM\_2; 1.  
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Query March 10.3%; Score 190.5; DB 13; Length 923;  
Best Local Similarity 27.6%; Pred. No. 2.1e-09;  
Matches 66; Conservative 29; Mismatches 95; Indels 49; Gaps 8;  
  
QY 5 GLILVTSALAGRRGTQAESNLSSKQFSSNKEQNGVDPQHERITVTSTNGSIHSRPF 64  
DB 12 GIFLIIVSALAKNDKCGDN-----IRITSANYLTSRCYF 43  
  
QY 65 HTVPRNTVLVRLVAVENWITQLTFDERFGLDEPEDDICKYDFVEVEEPPSD--GTLIGR 122  
DB 44 VSYTPSOKCIWITAPGNQRIILINFNPFDLEDRE--CKDYVEVVDGVDENGQLVGK 100  
  
QY 123 MCGSGTVPKQOISKNQIRIRFVSDEYFSPSEPGFCIHNYIMP-----OFTAVSPSVL 176  
DB 101 YCGK-IAPSPVSSGNQLFIFVSD-YETHGAGFSIRYEIFKTGPECSRNFPS--SSGVI 156  
  
QY 177 PPSALPLDLNNATTAFTLEDLIRYLEPERWQLDLEDLVPYTWQLGKAFVGRKSRV 235  
DB 157 KSPGFPEKYPNNLDCTFMIFAPKSEIVLEFSEFELEPDTP-----PAGVFCRYDRL 209

Search completed: May 27, 2004, 15:46:42  
Job time : 38.5 secs

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OM protein - protein search, using sw model

Run on: May 27, 2004, 15:42:51 ; Search time 16.5 Seconds  
(without alignments)  
1079.452 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLLSALAGQRTGT.....DVALEHHECDVCVCRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/2/1aa/5A COMB pep:\*
  - 2: /cgn2\_6/ptodata/2/1aa/5B COMB pep:\*
  - 3: /cgn2\_6/ptodata/2/1aa/6A COMB pep:\*
  - 4: /cgn2\_6/ptodata/2/1aa/6B COMB pep:\*
  - 5: /cgn2\_6/ptodata/2/1aa/PCITUS COMB pep:\*
  - 6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	4	US-09-457-066-43
2	1848	100.0	345	4	US-09-564-595D-35
3	1848	100.0	345	4	US-09-706-968-43
4	1848	100.0	345	4	US-09-823-033-4
5	1667	90.2	345	4	US-09-040-220D-2
6	1667	90.2	345	4	US-09-457-066-2
7	1667	90.2	345	4	US-09-265-686-2
8	1667	90.2	345	4	US-09-540-224-5
9	1667	90.2	345	4	US-09-564-595D-33
10	1667	90.2	345	4	US-09-706-968-2
11	1667	90.2	345	4	US-09-723-749-2
12	1667	90.2	345	4	US-09-823-033-2
13	1204.5	65.2	303	4	US-09-564-595D-57
14	1200	56.0	302	4	US-09-564-595D-54
15	1035.5	56.0	317	4	US-09-564-595D-56
16	1019	55.1	316	4	US-09-564-595D-55
17	752	40.7	370	4	US-09-457-066-37
18	752	40.7	370	4	US-09-540-224-2
19	752	40.7	370	4	US-09-564-595D-2
20	752	40.7	370	4	US-09-706-968-37
21	752	40.7	370	4	US-09-808-972-2
22	752	40.7	370	4	US-09-823-033-5
23	746.5	40.4	370	4	US-09-540-224-4
24	746.5	40.4	370	4	US-09-564-595D-53
25	746.5	40.4	370	4	US-09-808-972-4
26	185	10.0	1015	4	US-09-285-385C-2
27	183	9.9	1012	4	US-09-285-385C-4

28	181	9.8	788	1	US-08-572-225-1	Sequence 1, Appli
29	181	9.8	986	4	US-09-285-385C-19	Sequence 19, Appl
30	177.5	9.6	730	3	US-08-872-757-2	Sequence 2, Appli
31	177.5	9.6	730	4	US-09-850-048A-2	Sequence 2, Appli
32	176	9.5	923	4	US-09-439-711C-2	Sequence 2, Appli
33	176	9.5	923	4	US-09-563-638-2	Sequence 2, Appli
34	175	9.5	101	3	US-09-374-135-6	Sequence 6, Appli
35	172	9.3	922	4	US-09-116-473-4	Sequence 4, Appli
36	169	9.1	923	3	US-08-936-135-6	Sequence 6, Appli
37	169	9.1	923	4	US-09-439-711C-6	Sequence 6, Appli
38	168	9.1	921	4	US-09-439-711C-4	Sequence 4, Appli
39	168	9.1	986	3	US-08-872-757-4	Sequence 4, Appli
40	168	9.1	986	4	US-09-850-048A-4	Sequence 4, Appli
41	165	8.9	1013	2	US-08-866-650-3	Sequence 3, Appli
42	165	8.9	1013	2	US-09-021-287-3	Sequence 3, Appli
43	165	8.9	1013	3	US-09-240-473-3	Sequence 3, Appli
44	162	8.8	591	3	US-08-991-408-4	Sequence 4, Appli
45	162	8.8	591	4	US-09-432-473-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1					
US-09-457-066-43					
Sequence 43, Application US/09457066					
Patent No. 6432673					
GENERAL INFORMATION:					
APPLICANT: Gao, Zeren					
APPLICANT: Hart, Charles E.					
APPLICANT: Piddington, Christopher S.					
APPLICANT: Sheppard, Paul O.					
APPLICANT: Shoemaker, Kimberly E.					
APPLICANT: Gilbertson, Debra G.					
APPLICANT: West, James W.					
TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZYGF3					
FILE REFERENCE: 98-60					
CURRENT APPLICATION NUMBER: US/09/457,066					
CURRENT FILING DATE: 1999-12-07					
NUMBER OF SEQ ID NOS: 50					
SOFTWARE: FastSeq for Windows Version 3.0					
SEQ ID NO 43					
LENGTH: 345					
TYPE: PRT					
ORGANISM: Mus musculus					
US-09-457-066-43					
Query Match					
Best Local Similarity 100.0%; Score 1848; DB 4; Length 345;					
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MLLGLLLLSALAGQRTGTGTRAESNLSSKQLQSSDKQNGQVDPFRHRRVVTISGNGSIHS	60		
DB	1	MLLGLLLLSALAGQRTGTGTRAESNLSSKQLQSSDKQNGQVDPFRHRRVVTISGNGSIHS	60		
QY	61	PKPRHTYPRAMVLYMRLVANDENVRIQLTDERFGLEDDPDDICTKDFVEVEPSDDSVL	120		
DB	61	PKPRHTYPRAMVLYMRLVANDENVRIQLTDERFGLEDDPDDICTKDFVEVEPSDDSVL	120		
QY	121	GRMGSGTVGKQTSKGNHRIKRVFSDYPPSPGFCIHISIMPOVTEETSPSLVPPSS	180		
DB	121	GRMGSGTVGKQTSKGNHRIKRVFSDYPPSPGFCIHISIMPOVTEETSPSLVPPSS	180		
QY	181	LSLDLNNAVTAFSTLEELIRYLEPDRQVLDLSLYPTWQLLGAFLYKSKSRVNLNT	240		
DB	181	LSLDLNNAVTAFSTLEELIRYLEPDRQVLDLSLYPTWQLLGAFLYKSKSRVNLNT	240		
QY	241	LKEEVLYKSTPKNFSVIREELKRDITFWPCGLVYKRGNCACCLHNCNQCQVPRK	300		
DB	241	LKEEVLYKSTPKNFSVIREELKRDITFWPCGLVYKRGNCACCLHNCNQCQVPRK	300		
QY	301	VTKKYHEVLTLPKRTGVKGLKSLTDVALHHEECDCVCRGNAGG	345		
DB	301	VTKKYHEVLTLPKRTGVKGLKSLTDVALHHEECDCVCRGNAGG	345		

Db 301 VTKKHEVLQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345

## RESULT 2

US-09-564-595D-35

Sequence 35, Application US/09564595D

Patent No. 6495668

GENERAL INFORMATION:

APPLICANT: Gilbert, Teresa

APPLICANT: Hart, Charles E.

APPLICANT: Shepherd, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

FILE REFERENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/564,595D

PRIOR FILING DATE: 2000-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US 60/164,463

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 35

LENGTH: 345

TYPE: PRT

ORGANISM: Mus musculus

US-09-564-595D-35

Query Match

Best Local Similarity 100.0%; Score 1848; DB 4; Length 345;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLITSLAAGRTGTRAESENLSKQLQSSDKQKGVDPHRRVVTISGNGSIHS 60  
 1 MLILGLLITSLAAGRTGTRAESENLSKQLQSSDKQKGVDPHRRVVTISGNGSIHS 60  
 Db 61 PKFPHYPRNMVLVWRLVAVDENVRILQTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120  
 61 PKFPHYPRNMVLVWRLVAVDENVRILQTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120  
 QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDMQVDDLSLYKPTWOLLGKAFVIGKSKVNNL 240  
 181 LSLDLNNAVTAFTSTLEELIRYLEPDMQVDDLSLYKPTWOLLGKAFVIGKSKVNNL 240  
 Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300  
 241 LKEEVLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300  
 QY 301 VTKKHEVLQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345  
 301 VTKKHEVLQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345  
 Db 301 VTKKHEVLQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345

## RESULT 3

US-09-706-968-43

Sequence 43, Application US/09706968

Patent No. 6528050

GENERAL INFORMATION:

APPLICANT: Gao, Zeren

APPLICANT: Hart, Charles E.

APPLICANT: Piddington, Christopher S.

APPLICANT: Sheppard, Paul O.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Gilbertson, Debra G.

APPLICANT: West, James W.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

FILE REFERENCE: 98-60C1

CURRENT APPLICATION NUMBER: US/09/706, 968

CURRENT FILING DATE: 2000-11-06

PRIOR APPLICATION NUMBER: US/09/541, 752

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 43

LENGTH: 345

TYPE: PRT

ORGANISM: Mus musculus

US-09-706-968-43

Query Match

Best Local Similarity 100.0%; Score 1848; DB 4; Length 345;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLITSLAAGRTGTRAESENLSKQLQSSDKQKGVDPHRRVVTISGNGSIHS 60  
 1 MLILGLLITSLAAGRTGTRAESENLSKQLQSSDKQKGVDPHRRVVTISGNGSIHS 60  
 Db 61 PKFPHYPRNMVLVWRLVAVDENVRILQTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120  
 61 PKFPHYPRNMVLVWRLVAVDENVRILQTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120  
 QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDMQVDDLSLYKPTWOLLGKAFVIGKSKVNNL 240  
 181 LSLDLNNAVTAFTSTLEELIRYLEPDMQVDDLSLYKPTWOLLGKAFVIGKSKVNNL 240  
 Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300  
 241 LKEEVLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300  
 QY 301 VTKKHEVLQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345  
 301 VTKKHEVLQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345  
 Db 301 VTKKHEVLQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345

## RESULT 4

US-09-823-033-4

Sequence 4, Application US/09823033

Patent No. 6663870

GENERAL INFORMATION:

APPLICANT: Gilbertson, Debra G.

APPLICANT: Hart, Charles E.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

FILE REFERENCE: 00-12

CURRENT APPLICATION NUMBER: US/09/823, 033

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 345

TYPE: PRT

ORGANISM: Mus musculus

US-09-823-033-4

Query Match

Best Local Similarity 100.0%; Score 1848; DB 4; Length 345;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLITSLAAGRTGTRAESENLSKQLQSSDKQKGVDPHRRVVTISGNGSIHS 60  
 1 MLILGLLITSLAAGRTGTRAESENLSKQLQSSDKQKGVDPHRRVVTISGNGSIHS 60  
 Db 61 PKFPHYPRNMVLVWRLVAVDENVRILQTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120  
 61 PKFPHYPRNMVLVWRLVAVDENVRILQTFDERFGLEDEDDICKYDFVEVEEPPSDGSYL 120  
 QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180  
 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDYFPEPFGFCHYSIIMPVETTSPSVLPSS 180

```

Db      121 GRWGSGTVGKQSKGNHRIKRVSDPEYFSEBGFCHHSIIMPQVETTSPEVLPPSS 180
      181 LSLDLNNAVTAFTSEELIRYLEPDRWQVLDLSLYPTQQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAVTAFTSEELIRYLEPDRWQVLDLSLYPTQQLGKAPLYGKSKRYVNL 240
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIIPWGLLVKRCGNCACCLHNCNECQVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIIPWGLLVKRCGNCACCLHNCNECQVPRK 300
      301 VTKKYHEVLQLRPTGVGKLHKSITDVALHHEBECDCVCGNAG 345
      301 VTKKYHEVLQLRPTGVGKLHKSITDVALHHEBECDCVCGNAG 345

```

RESULT 5  
US-09-040-220D-2  
Sequence 2, Application US/09040220D  
Patent No. 6393311

```

GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
FILE REFERENCE: P1122
CURRENT APPLICATION NUMBER: US/09/040.220D
CURRENT FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-040-220D-2

```

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 5.5e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

```

Qy      1 MLLGLLLTSALAGQRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNSIHS 60
      1 MSLEGLLLTSALAGQRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNSIHS 60
      61 PKPHTYPRMVLVWRLVAVDENVRQLTDERFGLEDPEDDICKYDFVEVEBPSDGYL 120
      61 PRPHTYPRMVLVWRLVAVDENVRQLTDERFGLEDPEDDICKYDFVEVEBPSDGYL 120
      121 GRWGSGTVGKQSKGNHRIKRVSDPEYFSEBGFCHHSIIMPQVETTSPEVLPPSS 180
      121 GRWGSGTVGKQSKGNHRIKRVSDPEYFSEBGFCHHSIIMPQVETTSPEVLPPSS 180
      121 GRWGSGTVGKQSKGNHRIKRVSDPEYFSEBGFCHHSIIMPQVETTSPEVLPPSS 180
      181 LSLDLNNAVTAFTSEELIRYLEPDRWQVLDLSLYPTQQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAVTAFTSEELIRYLEPDRWQVLDLSLYPTQQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAVTAFTSEELIRYLEPDRWQVLDLSLYPTQQLGKAPLYGKSKRYVNL 240
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIIPWGLLVKRCGNCACCLHNCNECQVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIIPWGLLVKRCGNCACCLHNCNECQVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIIPWGLLVKRCGNCACCLHNCNECQVPRK 300
      301 VTKKYHEVLQLRPTGVGKLHKSITDVALHHEBECDCVCGNAG 345
      301 VTKKYHEVLQLRPTGVGKLHKSITDVALHHEBECDCVCGNAG 345
      301 VTKKYHEVLQLRPTGVGKLHKSITDVALHHEBECDCVCGNAG 345

```

RESULT 6  
US-09-457-066-2  
Sequence 2, Application US/09457066  
Patent No. 6432673  
GENERAL INFORMATION:  
APPLICANT: Geo. Zeren  
APPLICANT: Hart, Charles E.

```

APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457.066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-066-2

```

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 5.5e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

```

Qy      1 MLLGLLLTSALAGQRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNSIHS 60
      1 MSLEGLLLTSALAGQRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNSIHS 60
      61 PKPHTYPRMVLVWRLVAVDENVRQLTDERFGLEDPEDDICKYDFVEVEBPSDGYL 120
      61 PRPHTYPRMVLVWRLVAVDENVRQLTDERFGLEDPEDDICKYDFVEVEBPSDGYL 120
      121 GRWGSGTVGKQSKGNHRIKRVSDPEYFSEBGFCHHSIIMPQVETTSPEVLPPSS 180
      121 GRWGSGTVGKQSKGNHRIKRVSDPEYFSEBGFCHHSIIMPQVETTSPEVLPPSS 180
      121 GRWGSGTVGKQSKGNHRIKRVSDPEYFSEBGFCHHSIIMPQVETTSPEVLPPSS 180
      181 LSLDLNNAVTAFTSEELIRYLEPDRWQVLDLSLYPTQQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAVTAFTSEELIRYLEPDRWQVLDLSLYPTQQLGKAPLYGKSKRYVNL 240
      181 LSLDLNNAVTAFTSEELIRYLEPDRWQVLDLSLYPTQQLGKAPLYGKSKRYVNL 240
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIIPWGLLVKRCGNCACCLHNCNECQVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIIPWGLLVKRCGNCACCLHNCNECQVPRK 300
      241 LKEEVKLYSCTPRNFSVSIREBELKRTDTIIPWGLLVKRCGNCACCLHNCNECQVPRK 300
      301 VTKKYHEVLQLRPTGVGKLHKSITDVALHHEBECDCVCGNAG 345
      301 VTKKYHEVLQLRPTGVGKLHKSITDVALHHEBECDCVCGNAG 345
      301 VTKKYHEVLQLRPTGVGKLHKSITDVALHHEBECDCVCGNAG 345

```

RESULT 7  
US-09-265-686-2  
Sequence 2, Application US/09265686  
Patent No. 6455283

```

GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGY TO VEGF AND BMP1
FILE REFERENCE: P1122P2
CURRENT APPLICATION NUMBER: US/09/265.686
CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/040.220
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: US 09/184.216
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-265-686-2

```

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 5.5e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLTSALAGQRTGTRAESNLSKQLQSSDKQNGVQDPRHRRVVTISGNSIHS 60





PRIOR APPLICATION NUMBER: US/09/541,752  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-706-968-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 5.5e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGRTAENSLSKQLSDSKENGVODPRRHEVVTISNGSIHS 60  
DB 1 MSLFGLLLTSALAGORGTQAESNLSSKQFSSNKENGVDQDQHEHIIITVSTNGSIHS 60  
QY 61 PKPHTYPRNNVLVWRLVAVDENVRIQLTDFERFGLDEPDIDICKYDFVEVEEPPSDGSVL 120  
DB 61 PRPHITPRNTVLVWRLVAVDENVWIOITDFERFGLDEPDIDICKYDFVEVEEPPSDGTTIL 120  
QY 121 GRWCGSGTVPKGQTSKGNHRIIRFVSDEYFPSEBPGFCIHYSIIMPQVETTSPPSVLPSS 180  
DB 121 GRWCGSGTVPKGQTSKGNQIRIRFVSDEYFPSEBPGFCIHYNIVMPQTEAVSPSVLPESA 180  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVODLSLYKPTQQLGKAFLYGGKSKVYNLNTL 240  
DB 181 LPDLNNAITAFSTLEDLIRYLEPDRQVODLSLYKPTQQLGKAFLYGGKSKRVVDLNTL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIIPWPGCLLYKRCGNCACCLHNCNECQVPRK 300  
DB 241 LTBVRILYSCTPRNFVSIREELKRTDTIIPWPGCLLYKRCGNCACCLHNCNECQVPSK 300  
QY 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALBHHBECDCVCRGNAG 345  
DB 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALBHHBECDCVCRGSTG 345

RESULT 11  
US-09-723-749-2  
Sequence 2, Application US/09723749  
Patent No. 6620784  
GENERAL INFORMATION:  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
FILE REFERENCE: P1122P2D1  
CURRENT APPLICATION NUMBER: US/09/723,749  
CURRENT FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: US 09/265,686  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: US 09/040,220  
PRIOR FILING DATE: 1998-03-17  
PRIOR APPLICATION NUMBER: US 09/184,216  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 8  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Human  
US-09-723-749-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 5.5e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGRTAENSLSKQLSDSKENGVODPRRHEVVTISNGSIHS 60  
DB 1 MSLFGLLLTSALAGORGTQAESNLSSKQFSSNKENGVDQDQHEHIIITVSTNGSIHS 60  
QY 61 PKPHTYPRNNVLVWRLVAVDENVRIQLTDFERFGLDEPDIDICKYDFVEVEEPPSDGSVL 120  
DB 61 PRPHITPRNTVLVWRLVAVDENVWIOITDFERFGLDEPDIDICKYDFVEVEEPPSDGTTIL 120

DB 61 PRPHITPRNTVLVWRLVAVDENVWIOITDFERFGLDEPDIDICKYDFVEVEEPPSDGTTIL 120  
QY 121 GRWCGSGTVPKGQTSKGNHRIIRFVSDEYFPSEBPGFCIHYSIIMPQVETTSPPSVLPSS 180  
DB 121 GRWCGSGTVPKGQTSKGNQIRIRFVSDEYFPSEBPGFCIHYNIVMPQTEAVSPSVLPESA 180  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVODLSLYKPTQQLGKAFLYGGKSKVYNLNTL 240  
DB 181 LPDLNNAITAFSTLEDLIRYLEPDRQVODLSLYKPTQQLGKAFLYGGKSKRVVDLNTL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIIPWPGCLLYKRCGNCACCLHNCNECQVPRK 300  
DB 241 LTBVRILYSCTPRNFVSIREELKRTDTIIPWPGCLLYKRCGNCACCLHNCNECQVPSK 300  
QY 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALBHHBECDCVCRGNAG 345  
DB 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALBHHBECDCVCRGSTG 345

RESULT 12  
US-09-823-033-2  
Sequence 2, Application US/09823033  
Patent No. 6663870  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.  
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
FILE REFERENCE: 00-12  
CURRENT APPLICATION NUMBER: US/09/823,033  
CURRENT FILING DATE: 2001-03-29  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-823-033-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 5.5e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGRTAENSLSKQLSDSKENGVODPRRHEVVTISNGSIHS 60  
DB 1 MSLFGLLLTSALAGORGTQAESNLSSKQFSSNKENGVDQDQHEHIIITVSTNGSIHS 60  
QY 61 PKPHTYPRNNVLVWRLVAVDENVRIQLTDFERFGLDEPDIDICKYDFVEVEEPPSDGSVL 120  
DB 61 PRPHITPRNTVLVWRLVAVDENVWIOITDFERFGLDEPDIDICKYDFVEVEEPPSDGTTIL 120  
QY 121 GRWCGSGTVPKGQTSKGNHRIIRFVSDEYFPSEBPGFCIHYSIIMPQVETTSPPSVLPSS 180  
DB 121 GRWCGSGTVPKGQTSKGNQIRIRFVSDEYFPSEBPGFCIHYNIVMPQTEAVSPSVLPESA 180  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVODLSLYKPTQQLGKAFLYGGKSKVYNLNTL 240  
DB 181 LPDLNNAITAFSTLEDLIRYLEPDRQVODLSLYKPTQQLGKAFLYGGKSKRVVDLNTL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIIPWPGCLLYKRCGNCACCLHNCNECQVPRK 300  
DB 241 LTBVRILYSCTPRNFVSIREELKRTDTIIPWPGCLLYKRCGNCACCLHNCNECQVPSK 300  
QY 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALBHHBECDCVCRGNAG 345  
DB 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALBHHBECDCVCRGSTG 345

RESULT 13  
US-09-564-595D-57  
Sequence 57, Application US/09564595D  
Patent No. 6495668  
GENERAL INFORMATION:

```

; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57
```

```

Query Match          65.2%; Score 1204.5; DB 4; Length 303;
Best Local Similarity 71.3%; Pred. No. 4.3e-124;
Matches 216; Conservative 42; Mismatches 40; Indels 5; Gaps 3;

QY 47 ERVVTISGNGSIHSPKPHPTPRNMVLYWRLVAVDENVRIGQLTPDERGLEDDEDICKY 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 DETIQKNGYVQSPRPSPYRNLLITWLHS-QENTRIQLVFDNQFGLERENDICRY 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 107 DFEVEEPPSDGSLV--GRWCGSGTVPGKQTSKGNHIRFVSDYFSPSEPCIHYSIT- 163
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 DFEVEEDISRTSTIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFAKPGFKIYSLIE 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 164 -MPOVETTSPTLPPSSISLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOL 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 DFOPAASVSPVLPSPALPLDLNNATVAFSTLEDLIRYLEPDRQVLDLSLYKPTWOL 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 223 LGRAPLYGKSKVYNLNLKEEYKLYSCTPRNFSVSIREELKRTDTTFMPGCLLYKRCGG 282
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 LGRAPLYGKSKRVNDLNLKEEYKLYSCTPRNFSVSIREELKRTDTTFMPGCLLYKRCGG 240
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 283 NCACCLHNCNECCQVPRKTKYKHYEVLQLRPKTGVLKSLTDVALLEHHEBCDCVCRGN 342
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 NCACCLHNCNECCQVPSKTKYKHYEVLQLRPKTGVLKSLTDVALLEHHEBCDCVCRGS 300
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 343 AGG 345
   ||
Db 301 TGG 303
```

```

RESULT 14
US-09-564-595D-54
; Sequence 54, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
```

```

; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54
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```

Query Match          64.9%; Score 1200; DB 4; Length 302;
Best Local Similarity 72.4%; Pred. No. 1.3e-123;
Matches 215; Conservative 35; Mismatches 43; Indels 4; Gaps 2;

QY 46 HERVVTISGNGSIHSPKPHPTPRNMVLYWRLVAVDENVRIGQLTPDERGLEDDEDIC 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 HERIITVSTNGSIHSPKPHPTPRNMVLYWRLVAVDENVRIGQLTPDERGLEDDEDIC 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 106 YDFVEEPPSDGSLVLRWCGSGTVPGKQTSKGNHIRFVSDYFSPSEPCIHYSITMP 165
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YDFVEEPPSDGSLVLRWCGSGTVPGKQTSKGNHIRFVSDYFSPSEPCIHYSITMP 120
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 166 QVETTSPTLPPSSISLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOLGK 225
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 QVETTSPTLPPSSISLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOLGK 180
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 226 APLYGKSKVYNLNLKEEYKLYSCTPRNFSVSIREELKRTDTTFMPGCLLYKRCGCA 285
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 APLYGKSKSR-VLDLRLNDDAKRYSCTPRNYSVNIREELKLANVAFPPRCCLLYKRCGCG 239
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 286 CCLHNCNECCQVPRKTKYKHYEVLQLRPKTGVLKSLTDVALLEHHEBCDCVC 339
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 CGTVNRSCITCNSGKTKYKHYEVLQLRPKTGVLKSLTDVALLEHHEBCDCVC 296
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```

RESULT 15
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56
```

```

Query Match          56.0%; Score 1035.5; DB 4; Length 317;
Best Local Similarity 60.2%; Pred. No. 2e-105;
Matches 192; Conservative 47; Mismatches 57; Indels 23; Gaps 6;

QY 47 ERVVTISGNGSIHSPKPHPTPRNMVLYWRLVAVDENVRIGQLTPDERGLEDDEDIC 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 DETIQKNGYVQSPRPSPYRNLLITWLHS-QENTRIQLVFDNQFGLERENDICRY 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 107 DFEVEEPPSDGSLV--GRWCGSGTVPGKQTSKGNHIRFVSDYFSPSEPCIHYSIT- 163
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 DFEVEEDISRTSTIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFAKPGFKIYSLIE 120
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 164 -MPOVETTT-----SPSVLPSSISLDLNNAVTAFTLEELIRYLEPD 206
   |||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```

Db      121 DFQPAASETWESVTSISGVSYNSPSTDP-TLIADALDKIAEFTVEDLKYFNP 179
QY      207 RMQVLDLSLYKPTWQLGKAFLYGKKSKVYNLNLKEEVKLYSCTPRNFSYSIREELKRT 266
Db      180 SMQEDLENMYLDTPRYRGRSY-HDRKSKVVDLNLTEEVRLYSCTPRNFSYSIREELKRT 238
QY      267 DTIFMPCGLVYKRCGNCACCLHNCNECQCVPRKYTKKYHEVLOLRPKTGVGGLHKS LTD 326
Db      239 DTIFMPCGLVYKRCGNCACCLHNCNECQCVPSKYTKKYHEVLOLRPKTGVGGLHKS LTD 298
QY      327 VALEHHEBCDCVCRGNAGG 345
Db      299 VALEHHEBCDCVCRGSTGG 317

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Search completed: May 27, 2004, 15:48:09  
 Job time : 17.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:46:47 ; Search time 39 Seconds

(without alignments)  
2470.284 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848  
Sequence: 1 MLLLGILLTSALAGRTGT.....DVLEHHECDVCGRNAGG 345

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications AA:\*

- 1: /cgn2\_6/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/2/pubppaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/2/pubppaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/prodata/2/pubppaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/prodata/2/pubppaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/prodata/2/pubppaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/prodata/2/pubppaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/prodata/2/pubppaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/prodata/2/pubppaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/prodata/2/pubppaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/prodata/2/pubppaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/prodata/2/pubppaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/prodata/2/pubppaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	9	US-09-823-033-4
2	1848	100.0	345	9	US-09-818-943-2
3	1848	100.0	345	9	US-09-852-209A-7
4	1848	100.0	345	11	US-09-876-813-35
5	1848	100.0	345	12	US-10-664-432-4
6	1848	100.0	345	12	US-10-439-337A-7
7	1848	100.0	345	13	US-10-303-997B-7
8	1848	100.0	345	12	US-10-303-997B-7
9	1848	100.0	345	14	US-10-139-583-43
10	1848	100.0	345	14	US-10-131-600-7
11	1667	90.2	345	9	US-09-823-033-2
12	1667	90.2	345	9	US-09-923-995-4
13	1667	90.2	345	9	US-09-795-006A-149
14	1667	90.2	345	9	US-09-978-295A-488
15	1667	90.2	345	9	US-09-978-697-488

16	1667	90.2	345	9	US-09-978-192A-488	Sequence 488, App
17	1667	90.2	345	9	US-09-999-832A-488	Sequence 488, App
18	1667	90.2	345	10	US-09-978-189-488	Sequence 488, App
19	1667	90.2	345	10	US-09-796-753-6	Sequence 6, Appl1
20	1667	90.2	345	10	US-09-978-608A-488	Sequence 488, App
21	1667	90.2	345	10	US-09-978-585A-488	Sequence 488, App
22	1667	90.2	345	10	US-09-978-191A-488	Sequence 488, App
23	1667	90.2	345	10	US-09-978-403A-488	Sequence 488, App
24	1667	90.2	345	10	US-09-978-564A-488	Sequence 488, App
25	1667	90.2	345	10	US-09-999-833A-488	Sequence 488, App
26	1667	90.2	345	10	US-09-981-915A-488	Sequence 488, App
27	1667	90.2	345	10	US-09-978-824A-488	Sequence 488, App
28	1667	90.2	345	10	US-09-918-585A-488	Sequence 488, App
29	1667	90.2	345	10	US-09-978-423A-488	Sequence 488, App
30	1667	90.2	345	10	US-09-978-193A-488	Sequence 488, App
31	1667	90.2	345	10	US-09-999-830A-488	Sequence 488, App
32	1667	90.2	345	10	US-09-978-757A-488	Sequence 488, App
33	1667	90.2	345	10	US-09-978-187A-488	Sequence 488, App
34	1667	90.2	345	10	US-09-978-643A-488	Sequence 488, App
35	1667	90.2	345	10	US-09-978-375A-488	Sequence 488, App
36	1667	90.2	345	10	US-09-978-298A-488	Sequence 488, App
37	1667	90.2	345	10	US-09-978-188A-488	Sequence 488, App
38	1667	90.2	345	10	US-09-978-681A-488	Sequence 488, App
39	1667	90.2	345	10	US-09-978-194A-488	Sequence 488, App
40	1667	90.2	345	10	US-09-999-829A-488	Sequence 488, App
41	1667	90.2	345	10	US-09-978-299A-488	Sequence 488, App
42	1667	90.2	345	10	US-09-978-544A-488	Sequence 488, App
43	1667	90.2	345	10	US-09-978-665A-488	Sequence 488, App
44	1667	90.2	345	10	US-09-978-802A-488	Sequence 488, App
45	1667	90.2	345	11	US-09-876-813-33	Sequence 33, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-823-033-4  
Sequence 4, Application US/09823033  
Patent No. US2002004225A1  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.  
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
FILE REFERENCE: 00-12  
CURRENT FILING DATE: 2001-03-03  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-823-033-4

Query Match 100.0%; Score 1848; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLLGLLLTSALAGRTGT	RAESNLSSKQLQSSDKQNGVOPRHRVVTISNGSIHS	60
DB	1	MLLGLLLTSALAGRTGT	RAESNLSSKQLQSSDKQNGVOPRHRVVTISNGSIHS	60
QY	61	PKPHTYPRMVLVWRLVAVDENVR	IGLTFDERFGLEDPPDDICKYDFVEBPSDSVL	120
DB	61	PKPHTYPRMVLVWRLVAVDENVR	IGLTFDERFGLEDPPDDICKYDFVEBPSDSVL	120
QY	121	GRMGSGTVGKQTSKKNHRI	RVSDEYPPSEPGFCIHISIMPOVTETTSPPSS	180
DB	121	GRMGSGTVGKQTSKKNHRI	RVSDEYPPSEPGFCIHISIMPOVTETTSPPSS	180
QY	181	LSLDLNNATVAATSTEE	LTRYLEPPDMQVLDLSLYPTQGLGKAFLYKKKSQVNLN	240
DB	181	LSLDLNNATVAATSTEE	LTRYLEPPDMQVLDLSLYPTQGLGKAFLYKKKSQVNLN	240

Db 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLSYKPTWOLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNCNCCQCVPRK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNCNCCQCVPRK 300  
QY 301 VTKKYEVLQLRPKTGVKGLHKSLLDVALHHEBECDCVCRGNAG 345  
Db 301 VTKKYEVLQLRPKTGVKGLHKSLLDVALHHEBECDCVCRGNAG 345

## RESULT 2

US-09-818-943-2  
; Sequence 2, Application US/09818943  
; Patent No. US20020043987A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: LI, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: AASE, Karin  
; APPLICANT: LI, Hong  
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F  
; TITLE OF INVENTION: (PGF-C) AND USES THEREOF  
; FILE REFERENCE: 1064/48487  
; CURRENT APPLICATION NUMBER: US/09/818,943  
; CURRENT FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,507  
; PRIOR FILING DATE: 2000-03-28  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRF  
; ORGANISM: Murinae gen. sp.  
US-09-818-943-2

Query Match 100.0%; Score 1848; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLLTSLAAGRTGRTAASNLSSKQLQSSDKEQGVODPRHERVVTISGNSIHS 60  
Db 1 MLILGLLLTSLAAGRTGRTAASNLSSKQLQSSDKEQGVODPRHERVVTISGNSIHS 60  
QY 61 PKFPHTPYPRNMVLYMRLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEPSDGSYL 120  
Db 61 PKFPHTPYPRNMVLYMRLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEPSDGSYL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPSEPGFCIHYSIIMPQVTEITSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPSEPGFCIHYSIIMPQVTEITSPSVLPSS 180  
QY 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLSYKPTWOLLGKAFLYGKSKVNNL 240  
Db 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLSYKPTWOLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNCNCCQCVPRK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNCNCCQCVPRK 300  
QY 301 VTKKYEVLQLRPKTGVKGLHKSLLDVALHHEBECDCVCRGNAG 345  
Db 301 VTKKYEVLQLRPKTGVKGLHKSLLDVALHHEBECDCVCRGNAG 345

## RESULT 3

US-09-852-209A-7  
; Sequence 7, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri

; APPLICANT: PONTEN, Annica  
; APPLICANT: TUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 345  
; TYPE: PRF  
; ORGANISM: Murinae gen. sp.  
US-09-852-209A-7

Query Match 100.0%; Score 1848; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLILGLLLTSLAAGRTGRTAASNLSSKQLQSSDKEQGVODPRHERVVTISGNSIHS 60  
Db 1 MLILGLLLTSLAAGRTGRTAASNLSSKQLQSSDKEQGVODPRHERVVTISGNSIHS 60  
QY 61 PKFPHTPYPRNMVLYMRLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEPSDGSYL 120  
Db 61 PKFPHTPYPRNMVLYMRLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEPSDGSYL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPSEPGFCIHYSIIMPQVTEITSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPSEPGFCIHYSIIMPQVTEITSPSVLPSS 180  
QY 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLSYKPTWOLLGKAFLYGKSKVNNL 240  
Db 181 LSLDLNNAVTAESTLEELIRYLEPDRWQVLDLSYKPTWOLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNCNCCQCVPRK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGACCLHNCNCCQCVPRK 300  
QY 301 VTKKYEVLQLRPKTGVKGLHKSLLDVALHHEBECDCVCRGNAG 345  
Db 301 VTKKYEVLQLRPKTGVKGLHKSLLDVALHHEBECDCVCRGNAG 345

## RESULT 4

US-09-876-813-35  
; Sequence 35, Application US/09876813  
; Publication No. US20040002140A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZW694  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216

;; PRIOR FILING DATE: 1999-05-03  
;; PRIOR APPLICATION NUMBER: US 60/164,463  
;; PRIOR FILING DATE: 1999-11-10  
;; PRIOR APPLICATION NUMBER: US 60/180,169  
;; PRIOR FILING DATE: 2000-02-04  
;; NUMBER OF SEQ ID NOS: 57  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 35  
;; LENGTH: 345  
;; TYPE: PRN  
;; ORGANISM: Mus musculus  
US-09-876-813-35

Query Match 100.0%; Score 1848; DB 11; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
DB 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
QY 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLDPEDDICKYDFVEVEBPSDGSVL 120  
DB 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLDPEDDICKYDFVEVEBPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBGFCHYSIIMPQVETTSPTVLPSS 180  
DB 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBGFCHYSIIMPQVETTSPTVLPSS 180  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKSVNMLN 240  
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKSVNMLN 240  
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTIFFPGCLLYKRCGNCACCLHNCNCCQVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIRELKRDTTIFFPGCLLYKRCGNCACCLHNCNCCQVPRK 300  
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345  
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345

RESULT 5  
US-10-664-432-4  
;; Sequence 4, Application US/10664432  
;; Publication No. US20040043031A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Hart, Charles E.  
;; APPLICANT: Gilbertson, Debra G.  
;; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
;; FILE REFERENCE: 00-12  
;; CURRENT APPLICATION NUMBER: US/10/664,432  
;; CURRENT FILING DATE: 2003-09-19  
;; NUMBER OF SEQ ID NOS: 5  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 4  
;; LENGTH: 345  
;; TYPE: PRN  
;; ORGANISM: Mus musculus  
US-10-664-432-4

Query Match 100.0%; Score 1848; DB 12; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
DB 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
QY 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLDPEDDICKYDFVEVEBPSDGSVL 120  
DB 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLDPEDDICKYDFVEVEBPSDGSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBGFCHYSIIMPQVETTSPTVLPSS 180  
DB 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBGFCHYSIIMPQVETTSPTVLPSS 180  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKSVNMLN 240  
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKSKSVNMLN 240  
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTIFFPGCLLYKRCGNCACCLHNCNCCQVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIRELKRDTTIFFPGCLLYKRCGNCACCLHNCNCCQVPRK 300  
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345  
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345

RESULT 6  
US-10-439-337A-7  
;; Sequence 7, Application US/10439337A  
;; Publication No. US20040053837A1  
;; GENERAL INFORMATION:  
;; APPLICANT: LI, Xuri  
;; APPLICANT: ERIKSSON, Ulf  
;; APPLICANT: CARMELET, Peter  
;; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND  
;; FILE REFERENCE: 029065.44740C4  
;; CURRENT APPLICATION NUMBER: US/10/439,337A  
;; PRIOR FILING DATE: 2003-05-16  
;; PRIOR APPLICATION NUMBER: US 10/303,997  
;; PRIOR FILING DATE: 2002-11-26  
;; PRIOR APPLICATION NUMBER: US 09/410,349  
;; PRIOR FILING DATE: 1999-09-30  
;; PRIOR APPLICATION NUMBER: US 60/102,461  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: US 60/108,109  
;; PRIOR FILING DATE: 1998-11-12  
;; PRIOR APPLICATION NUMBER: US 60/110,749  
;; PRIOR FILING DATE: 1998-12-03  
;; PRIOR APPLICATION NUMBER: US 60/113,002  
;; PRIOR FILING DATE: 1998-12-18  
;; PRIOR APPLICATION NUMBER: US 60/135,426  
;; PRIOR FILING DATE: 1999-05-21  
;; PRIOR APPLICATION NUMBER: US 60/144,022  
;; PRIOR FILING DATE: 1999-07-15  
;; NUMBER OF SEQ ID NOS: 40  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 7  
;; LENGTH: 345  
;; TYPE: PRN  
;; ORGANISM: Murinae gen. sp.  
US-10-439-337A-7

Query Match 100.0%; Score 1848; DB 12; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
DB 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
QY 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLDPEDDICKYDFVEVEBPSDGSVL 120  
DB 61 PKPHTYPRNNVLYWRLVAVDENVRIOQLTDERFGLDPEDDICKYDFVEVEBPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBGFCHYSIIMPQVETTSPTVLPSS 180  
DB 121 GRWCGSGTVPGKQTSKGNHRIREFVSDYFPEBGFCHYSIIMPQVETTSPTVLPSS 180  
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345  
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVALHEHBECDVCRCNAGG 345

Db 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLN 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300  
QY 301 VTKKHEVLOLRPKTVGKGLHKSITDVALHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLOLRPKTVGKGLHKSITDVALHHEECDCVCRGNAGG 345  
  
RESULT 7  
US-10-303-997B-7  
; Sequence 7, Application US/10303997B  
; Publication No. US20030211994A1  
; GENERAL INFORMATION:  
; APPLICANT: LI, Xuri  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: CARMELIET, Peter  
; APPLICANT: COLLUM, Desire  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN  
; FILE REFERENCE: 029065.44740C3  
; CURRENT APPLICATION NUMBER: US/10/303, 997B  
; PRIOR FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: US 60/102,461  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: US 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 64/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: US 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: US 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-10-303-997B-7  
  
Query Match 100.0%; Score 1848; DB 12; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLILGLLLTSALAGRTGTRAESNLSSKQLQSSDKONGVODPRHERVVTISGNSIHS 60  
Db 1 MLILGLLLTSALAGRTGTRAESNLSSKQLQSSDKONGVODPRHERVVTISGNSIHS 60  
QY 61 PKPHTYPRNMVLYWRLVAVDENVRQLTFDERFGLEDDEDDICKYDFVEVEEPPSDGSYL 120  
Db 61 PKPHTYPRNMVLYWRLVAVDENVRQLTFDERFGLEDDEDDICKYDFVEVEEPPSDGSYL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPBPGFCIHYSIIMPVTEETSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPBPGFCIHYSIIMPVTEETSPSVLPSS 180  
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLN 240  
Db 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLN 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300  
QY 301 VTKKHEVLOLRPKTVGKGLHKSITDVALHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLOLRPKTVGKGLHKSITDVALHHEECDCVCRGNAGG 345

Db 301 VTKKHEVLOLRPKTVGKGLHKSITDVALHHEECDCVCRGNAGG 345  
  
RESULT 8  
US-10-139-583-43  
; Sequence 43, Application US/10139583  
; Publication No. US20020177193A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/10/139,583  
; PRIOR FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 09/457,066  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-139-583-43  
  
Query Match 100.0%; Score 1848; DB 13; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLILGLLLTSALAGRTGTRAESNLSSKQLQSSDKONGVODPRHERVVTISGNSIHS 60  
Db 1 MLILGLLLTSALAGRTGTRAESNLSSKQLQSSDKONGVODPRHERVVTISGNSIHS 60  
QY 61 PKPHTYPRNMVLYWRLVAVDENVRQLTFDERFGLEDDEDDICKYDFVEVEEPPSDGSYL 120  
Db 61 PKPHTYPRNMVLYWRLVAVDENVRQLTFDERFGLEDDEDDICKYDFVEVEEPPSDGSYL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPBPGFCIHYSIIMPVTEETSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPBPGFCIHYSIIMPVTEETSPSVLPSS 180  
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLN 240  
Db 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKSVNLN 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFMPCGLVYKRGCGNACCLHNCCGCVPRK 300  
QY 301 VTKKHEVLOLRPKTVGKGLHKSITDVALHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLOLRPKTVGKGLHKSITDVALHHEECDCVCRGNAGG 345  
  
RESULT 9  
US-10-131-600-7  
; Sequence 7, Application US/10131600  
; Publication No. US20030082670A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: FONTEN, Annica  
; APPLICANT: UTTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christler  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING



TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
CURRENT APPLICATION NUMBER: US/10/131,600  
CURRENT FILING DATE: 2002-04-25  
PRIOR APPLICATION NUMBER: US/09/410,349  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 60/108,109  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: 60/110,749  
PRIOR FILING DATE: 1998-12-03  
PRIOR APPLICATION NUMBER: 60/113,002  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: 60/135,426  
PRIOR FILING DATE: 1999-05-21  
PRIOR APPLICATION NUMBER: 60/144,022  
PRIOR FILING DATE: 1999-07-15  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 7  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Murinae gen. sp.  
US-10-131-600-7

Query Match 100.0%; Score 1848; DB 14; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1,3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
DB 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
QY 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERFGLBDEPDICKYDFVEVEEBSDSVL 120  
DB 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERFGLBDEPDICKYDFVEVEEBSDSVL 120  
QY 121 GRMGSGTVPGKQTSKGNHRIIRFVSDYFPESEPGFCHYSIIMPQVETTSPTVLPSS 180  
DB 121 GRMGSGTVPGKQTSKGNHRIIRFVSDYFPESEPGFCHYSIIMPQVETTSPTVLPSS 180  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOLGKAPLYGKSKVNLNTL 240  
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOLGKAPLYGKSKVNLNTL 240  
QY 241 LKEEVKLYSCTPRNFVSISIRELKRDTTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300  
DB 241 LKEEVKLYSCTPRNFVSISIRELKRDTTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300  
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVLEHHEBCDCVCRGNAGG 345  
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVLEHHEBCDCVCRGNAGG 345

RESULT 10  
US-10-264-361-4  
Sequence 4, Application US/10264361  
Publication No. US20030087870A1  
GENERAL INFORMATION:  
APPLICANT: Gilbertson, Debra G.  
TITLE OF INVENTION: METHOD OF TREATING FIBROSIS  
FILE REFERENCE: 00-53  
CURRENT APPLICATION NUMBER: US/10/264,361  
PRIOR FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: US/09/695,121  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-264-361-4

Query Match 100.0%; Score 1848; DB 14; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1,3e-173;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
DB 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
QY 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERFGLBDEPDICKYDFVEVEEBSDSVL 120  
DB 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERFGLBDEPDICKYDFVEVEEBSDSVL 120  
QY 121 GRMGSGTVPGKQTSKGNHRIIRFVSDYFPESEPGFCHYSIIMPQVETTSPTVLPSS 180  
DB 121 GRMGSGTVPGKQTSKGNHRIIRFVSDYFPESEPGFCHYSIIMPQVETTSPTVLPSS 180  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOLGKAPLYGKSKVNLNTL 240  
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOLGKAPLYGKSKVNLNTL 240  
QY 241 LKEEVKLYSCTPRNFVSISIRELKRDTTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300  
DB 241 LKEEVKLYSCTPRNFVSISIRELKRDTTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300  
QY 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVLEHHEBCDCVCRGNAGG 345  
DB 301 VTKKYHEVLOLRPKTVGKGLHKSLLTDVLEHHEBCDCVCRGNAGG 345

RESULT 11  
US-09-823-033-2  
Sequence 2, Application US/09823033  
Patent No. US2002004225A1  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.  
APPLICANT: Gilbertson, Debra G.  
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
FILE REFERENCE: 00-12  
CURRENT APPLICATION NUMBER: US/09/823,033  
PRIOR FILING DATE: 2001-03-29  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-823-033-2

Query Match 90.2%; Score 1667; DB 9; Length 345;  
Best Local Similarity 87.0%; Pred. No. 9.9e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
DB 1 MLLGLLLTSALAGORTGRTAESNLSSKQLSSDKONGVODPRHERVVTISGNGSIHS 60  
QY 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERFGLBDEPDICKYDFVEVEEBSDSVL 120  
DB 61 PKPHTYPRNMVWLVRVAVDENVRIOQLTDERFGLBDEPDICKYDFVEVEEBSDSVL 120  
QY 121 GRMGSGTVPGKQTSKGNHRIIRFVSDYFPESEPGFCHYSIIMPQVETTSPTVLPSS 180  
DB 121 GRMGSGTVPGKQTSKGNHRIIRFVSDYFPESEPGFCHYSIIMPQVETTSPTVLPSS 180  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOLGKAPLYGKSKVNLNTL 240  
DB 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWOLGKAPLYGKSKVNLNTL 240  
QY 241 LKEEVKLYSCTPRNFVSISIRELKRDTTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300  
DB 241 LKEEVKLYSCTPRNFVSISIRELKRDTTIFWPGCLLYKRCGNCACCLHNCNECCVPRK 300

QY 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHHEBECDCVCRGNAG 345  
 Db 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHHEBECDCVCRGNAG 345

RESULT 12  
 US-09-923-995-4  
 ; Sequence 4, Application US/09923995  
 ; Patent No. US20020081700A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shepard, Paul O  
 ; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNKL  
 ; FILE REFERENCE: 00-47  
 ; CURRENT APPLICATION NUMBER: US/09/923,995  
 ; CURRENT FILING DATE: 2001-08-07  
 ; PRIOR APPLICATION NUMBER: US 60/223,164  
 ; PRIOR FILING DATE: 2000-08-07  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 345  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-923-995-4

Query Match 90.2%; Score 1667; DB 9; Length 345;  
 Best Local Similarity 87.0%; Pred. No. 9,9e-156;  
 Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLILGLLITSLAAGRTGTRAEASNLSKQLQSSDKQNGVDPRIHRRVTTISGNSIHS 60  
 Db 1 MSIFGLLITSLAAGRGQTQAESNLSKQFSSNKQNGVDPRIHRRVTTISGNSIHS 60  
 QY 61 PKPHTYPRNMVLVWRLVAVDENVRQLQTFDERFGLEDEDDICXDFVEVEEPPSGSVL 120  
 Db 61 PREPHTYPRNTVLMRLVAVDENVRQLQTFDERFGLEDEDDICXDFVEVEEPPSGSVL 120  
 QY 121 GRWCGSTVPKQTSKGNHIRIRFVSDEYFPPSPGFCIHYSIMPOVETTSFVLPSS 180  
 Db 121 GRWCGSTVPKQTSKGNQIRIRFVSDEYFPPSPGFCIHYNIMPOTEAVSPVLPSS 180  
 QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTMOLIGKAFYGRKSRVVDLNL 240  
 Db 181 LPIDLNNAITAFSTLEDLIRYLEPDRWQVDLSLYKPTMOLIGKAFVFGKSRVVDLNL 240  
 QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCQCVPRK 300  
 Db 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCQCVPRK 300  
 QY 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHHEBECDCVCRGNAG 345  
 Db 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHHEBECDCVCRGNAG 345

RESULT 13  
 US-09-795-006A-149  
 ; Sequence 149, Application US/09795006A  
 ; Patent No. US20020151680A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alitalo et al  
 ; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
 ; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS  
 ; FILE REFERENCE: 28967/35977B  
 ; CURRENT APPLICATION NUMBER: US/09/795,006A  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: US 60/205,331  
 ; PRIOR FILING DATE: 2000-05-18  
 ; PRIOR APPLICATION NUMBER: US 60/185,205  
 ; PRIOR FILING DATE: 2000-02-25  
 ; NUMBER OF SEQ ID NOS: 175  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 149  
 ; LENGTH: 345

TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-795-006A-149

Query Match 90.2%; Score 1667; DB 9; Length 345;  
 Best Local Similarity 87.0%; Pred. No. 9,9e-156;  
 Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLILGLLITSLAAGRTGTRAEASNLSKQLQSSDKQNGVDPRIHRRVTTISGNSIHS 60  
 Db 1 MSIFGLLITSLAAGRGQTQAESNLSKQFSSNKQNGVDPRIHRRVTTISGNSIHS 60  
 QY 61 PKPHTYPRNMVLVWRLVAVDENVRQLQTFDERFGLEDEDDICXDFVEVEEPPSGSVL 120  
 Db 61 PREPHTYPRNTVLMRLVAVDENVRQLQTFDERFGLEDEDDICXDFVEVEEPPSGSVL 120  
 QY 121 GRWCGSTVPKQTSKGNHIRIRFVSDEYFPPSPGFCIHYSIMPOVETTSFVLPSS 180  
 Db 121 GRWCGSTVPKQTSKGNQIRIRFVSDEYFPPSPGFCIHYNIMPOTEAVSPVLPSS 180  
 QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVDLSLYKPTMOLIGKAFYGRKSRVVDLNL 240  
 Db 181 LPIDLNNAITAFSTLEDLIRYLEPDRWQVDLSLYKPTMOLIGKAFVFGKSRVVDLNL 240  
 QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCQCVPRK 300  
 Db 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECCQCVPRK 300  
 QY 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHHEBECDCVCRGNAG 345  
 Db 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHHEBECDCVCRGNAG 345

RESULT 14  
 US-09-978-295A-488  
 ; Sequence 488, Application US/09978295A  
 ; Patent No. US2002015606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerlitsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumes, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C11  
 ; CURRENT APPLICATION NUMBER: US/09/978,295A  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250

[illegible]

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/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match          90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 9, 9e-156;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLILGLILTSALAGORTGRASNLSSKQLSDSKONGVODPRHRVVTISGNSIHS 60
DB 1 MSIFGLILTSALAGORQAGQAGQESNLSSKQFSSNKEQNGVDPQHERITVTSNGSIHS 60
QY 61 PKRPHTYPRNMVLMRLVAVDENVRILQTFDERFGLDEPDIDICKYDFVEEPPSDGSYL 120
DB 61 PRPHYPRNTVLMRLVAVENVRILQTFDERFGLDEPDIDICKYDFVEEPPSDGSYL 120
QY 121 GRMGSGTVPGKQTSKKNHIRIRFVSDYPPSPGFCIHSIMPOVETTSVLPSS 180
DB 121 GRMGSGTVPGKQTSKKNHIRIRFVSDYPPSPGFCIHSIMPOVETTSVLPSS 180
QY 181 LSLDLNNATVASTLEELRYLEPDRQVLDLSIKPTMQLGKFLYKSKVNLN 240
DB 181 LSLDLNNATVASTLEELRYLEPDRQVLDLSIKPTMQLGKFLYKSKVNLN 240
QY 241 LKEEVLYSCTPRNFSVIRIELKRTDTTFMPCGLVYKCGNACCLHNHCNQCQVPRK 300
DB 241 LKEEVLYSCTPRNFSVIRIELKRTDTTFMPCGLVYKCGNACCLHNHCNQCQVPRK 300
QY 301 VTKKYEHLQLRPKTVGKGLKSLTDVLEHHECCVCGNAGG 345
DB 301 VTKKYEHLQLRPKTVGKGLKSLTDVLEHHECCVCGNAGG 345

RESULT 15
US-09-978-697-488
/ Sequence 488, Application US/09978697
/ Patent No. US20020169284A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerlitsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James J.
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
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/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C27
/ CURRENT APPLICATION NUMBER: US/09/978,697
/ PRIOR APPLICATION NUMBER: 2001-10-16
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.2%; Score 1667; DB 9; Length 345;  
Best Local Similarity 87.0%; Pred. No. 9.9e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLILTSALAGRTGTRAESNLSSKQLSSDKQNGVDPFRHRRVVTISGNGSIHS 60  
Db 1 MSLLGLILTSALAGRTGTRAESNLSSKQLSSDKQNGVDPFRHRRVVTISGNGSIHS 60  
Qy 61 PKPHTYPRNMTVLRVAVDENVRIOTLTDERFGLDPEDDICKYFVEEESDGSVL 120  
Db 61 PRPHTYPRNMTVLRVAVDENVRIOTLTDERFGLDPEDDICKYFVEEESDGSVL 120  
Qy 121 GRWGSSTVPQKQSKNHRIRFVSDYEPSEBGFCHYSIIMPOVETTTSPVLPPSS 180  
Db 121 GRWGSSTVPQKQSKNHRIRFVSDYEPSEBGFCHYSIIMPOVETTTSPVLPPSS 180  
Qy 181 LSLDLNNAVTAFTLEELIRYLEPDRQVLDLSYKPTQQLGKAPLYGKSKRVNMLNL 240  
Db 181 LPLDLNNAVTAFTLEELIRYLEPDRQVLDLSYKPTQQLGKAPLYGKSKRVNMLNL 240  
Qy 241 LKEEVKLYSCTPRNFSVSIRELKRDTITFPGLVRCGACCAACCLANCNQCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIRELKRDTITFPGLVRCGACCAACCLANCNQCQVPRK 300  
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Db 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHHEHCDCVCGNNGG 345

Search completed: May 27, 2004, 15:56:27  
Job time : 40 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:37:31 ; Search time 51 Seconds  
(without alignments)  
1911.351 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLTSLALAGQRRTG.....DVALEHRECDVCGRNAGC 345

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*\n2: Geneseqp1990s:\*\n3: Geneseqp2000s:\*\n4: Geneseqp2001s:\*\n5: Geneseqp2002s:\*\n6: Geneseqp2003as:\*\n7: Geneseqp2003bs:\*\n8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1848	100.0	345	AAy96861	AAy96861 Murine va
3	1848	100.0	345	AAy84858	AAy84858 Mouse zve
4	1848	100.0	345	AAy84858	AAy84858 Mouse zve
5	1848	100.0	345	AAy84858	AAy84858 Mouse zve
6	1848	100.0	345	AAy84858	AAy84858 Mouse zve
7	1848	100.0	345	AAy84858	AAy84858 Mouse zve
8	1848	100.0	345	AAy84858	AAy84858 Mouse zve
9	1848	100.0	345	AAy84858	AAy84858 Mouse zve
10	1848	100.0	345	AAy84858	AAy84858 Mouse zve
11	1848	100.0	345	AAy84858	AAy84858 Mouse zve
12	1848	100.0	345	AAy84858	AAy84858 Mouse zve
13	1848	100.0	345	AAy84858	AAy84858 Mouse zve
14	1848	100.0	345	AAy84858	AAy84858 Mouse zve
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18	1848	100.0	345	AAy84858	AAy84858 Mouse zve
19	1848	100.0	345	AAy84858	AAy84858 Mouse zve
20	1848	100.0	345	AAy84858	AAy84858 Mouse zve
21	1848	100.0	345	AAy84858	AAy84858 Mouse zve
22	1848	100.0	345	AAy84858	AAy84858 Mouse zve
23	1848	100.0	345	AAy84858	AAy84858 Mouse zve
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31	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
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33	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
34	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
35	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
36	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
37	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
38	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
39	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
40	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
41	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
42	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
43	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
44	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.
45	1667	90.2	345	4	AAy84559	AAy84559 standard; protein, 345 AA.

## ALIGNMENTS

RESULT 1	AAy84559	AAy84559 standard; protein, 345 AA.	AAy84559
ID	AAy84559	AAy84559 standard; protein, 345 AA.	AAy84559
AC	AAy84559	AAy84559 standard; protein, 345 AA.	AAy84559
DT	25-JUL-2000	(first entry)	25-JUL-2000
DE	A murine platelet-derived growth factor C (PDGF-C).		
XX	Platelet-derived growth factor C; PDGF-C; cell proliferation;		
XX	growth factor; heparin; connective tissue; wound healing; VEGF-F;		
XX	fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;		
XX	choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;		
XX	lung carcinoma; erythroleukemia; tissue remodelling.		
OS	Mus sp.		
XX	WO200018212-A2.		
XX	06-APR-2000.		
XX	30-SEP-1999; 99WO-US022668.		
XX	30-SEP-1998; 98US-0102461P.		
XX	12-NOV-1998; 98US-0108109P.		
XX	03-DEC-1998; 98US-0110749P.		
XX	18-DEC-1998; 98US-0113002P.		
XX	21-MAY-1999; 99US-0135426P.		
XX	15-JUL-1999; 99US-0144022P.		
XX	(LUDM-) LUDMIG INST CANCER RES.		
XX	(UYHE-) UNIV HELSINKI LICENSING LTD.		
XX	Eriksson U, Aase K, Ponten A, Uutela M, Alltalo K;		
XX	Oestman A, Heldin C, Betsholtz C;		
XX	WPI; 2000-292954/25.		
XX	N-PSDB; AAA12525.		
XX	Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,		
XX	differentiation, growth and motility of cells expressing the PDGF-C		
XX	receptor.		
XX	Claim 27; Fig 6; 135pp; English.		
XX	The present sequence represents murine platelet-derived growth factor C		
XX	(PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the		

CC ability to stimulate and enhance proliferation or differentiation, and/or  
CC growth or motility of cells expressing a PDGF-C receptor. PDGF-C  
CC polypeptides can be used in pharmaceuticals for promoting cell  
CC proliferation, preferably in combination with one other growth factor and  
CC heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used  
CC for stimulating connective tissue or wound healing. The PDGF-C  
CC polypeptide can be enzymatically processed to generate the active  
CC truncated form of PDGF-C and used to regulate the receptor-binding  
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast  
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.  
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour  
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.  
CC chorioadenoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma  
CC and erythroleukemia, can be identified by testing for expression of PDGF-  
CC C. PDGF-C antagonists can also be used to inhibit tissue remodelling  
CC during invasion of tumour cells into a normal population of cells.  
CC Antagonists can also be used to treat fibrotic conditions, especially  
CC found in the lung, kidney or liver

XX  
XX Sequence 345 AA;  
SQ

Query Match 100.0%; Score 1848; DB 3; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.8e-181;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSLAGRTGTRASNLSSKQLSSDKQNGVDPRRERVTTISGNSIHS 60  
1 MLLIGLLLTSLAGRTGTRASNLSSKQLSSDKQNGVDPRRERVTTISGNSIHS 60  
DB 1 MLLIGLLLTSLAGRTGTRASNLSSKQLSSDKQNGVDPRRERVTTISGNSIHS 60

QY 61 PKPHTYPRNMVLTWRLVAVDENVRQLTFDERFGLEDDEDDICKDFVEVEPSDGSVL 120  
61 PKPHTYPRNMVLTWRLVAVDENVRQLTFDERFGLEDDEDDICKDFVEVEPSDGSVL 120  
DB 61 PKPHTYPRNMVLTWRLVAVDENVRQLTFDERFGLEDDEDDICKDFVEVEPSDGSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHRIKRVSDSEYFSPGFCIHYSITMPVTTETSPSVLPSS 180  
121 GRWCGSGTVPGKQTSKGNHRIKRVSDSEYFSPGFCIHYSITMPVTTETSPSVLPSS 180  
DB 121 GRWCGSGTVPGKQTSKGNHRIKRVSDSEYFSPGFCIHYSITMPVTTETSPSVLPSS 180

QY 181 LSLDLNNNAVTAFTSTLEELIRYLEPRWQVLDLSLYKPTWQLGKAFLYGKSKVNLNL 240  
181 LSLDLNNNAVTAFTSTLEELIRYLEPRWQVLDLSLYKPTWQLGKAFLYGKSKVNLNL 240  
DB 181 LSLDLNNNAVTAFTSTLEELIRYLEPRWQVLDLSLYKPTWQLGKAFLYGKSKVNLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLANECQCVPK 300  
241 LKEEVKLYSCTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLANECQCVPK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLANECQCVPK 300

QY 301 VTKKYEHLQLRPKTVGKGLKSLTDVALHEHEECDCVCRGNAGG 345  
301 VTKKYEHLQLRPKTVGKGLKSLTDVALHEHEECDCVCRGNAGG 345  
DB 301 VTKKYEHLQLRPKTVGKGLKSLTDVALHEHEECDCVCRGNAGG 345

RESULT 2  
AA96861  
ID AA96861 standard; protein; 345 AA.  
XX  
AC AA96861;  
XX  
DT 26-SEP-2000 (first entry)  
XX  
DE Murine vascular endothelial growth factor homologue, ZVEGF3.  
XX  
KW Vascular endothelial growth factor; homologue; zvegf3; CUB domain;  
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;  
KW chromosome 4q28.3; cytosolic; anti-psoriatic; anti-inflammatory;  
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;  
KW vulnerability.  
XX  
OS Mus musculus.  
XX  
PN MO200034474-A2.  
XX  
PD 15-JUN-2000.  
XX  
PF 07-DEC-1999; 99WO-US028968.

XX 07-DEC-1998; 98US-00207120.  
PR 06-JUN-1999; 99US-0142576P.  
PR 21-OCT-1999; 99US-016153P.  
PR 12-NOV-1999; 99US-0165255P.  
XX  
PA (ZYMO) ZYMOGENETICS INC.  
PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE,  
PI Gilbartson DG, West JW;  
XX WPI, 2000-423420/36.  
DR N-PSDB; AAA51527.  
XX  
XX Novel zvegf3 polypeptides and nucleotides encoding them useful for  
PT stimulating growth of smooth muscle cells and fibroblasts comprising an  
PT epitope bearing portion of a specific amino acid sequence.  
XX  
PS Claim 1; Page 169-170; 173pp; English.  
XX  
XX This shows a murine ZVEGF3 a novel vascular endothelial growth factor  
CC homologue. Polypeptides comprising an epitope-bearing portion human or  
CC murine ZVEGF3 are claimed. The growth factors comprise a growth factor  
CC domain and a CUB domain (generic sequence motifs are shown in AA96859  
CC and AA96860). The growth factor domain is characterized by an  
CC arrangement of cysteine residues and beta-strands that is characteristic  
CC of the "cysteine knot" structure of the platelet-derived growth factor  
CC (PDGF) family. The CUB domain shows homology to CUB domains in  
CC neuropilin, human bone morphogenetic protein-1, porcine seminal plasma  
CC protein, bovine acidic seminal fluid protein and Xenopus laevis collagen-  
CC like protein. Structural analysis and homology predict that ZVEGF3  
CC polypeptides complex with a second polypeptide to form multimeric  
CC proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.  
CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth  
CC muscle cells, for activating cell surface PDGF-alpha receptor and for  
CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is  
CC useful for regulating (post-development) organ growth, regeneration and  
CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3  
CC antagonists are useful for treating cancer, rheumatoid arthritis,  
CC diabetic retinopathy, ischemic limb disease, peripheral vascular disease,  
CC myocardial ischemia, vascular intimal hyperplasia, atherosclerosis, wound  
CC healing, chronic liver disease and haemangioma formation. ZVEGF3 can also  
CC be used to modulate neurite growth and development of the nervous system,  
CC and for treating neurodegenerative diseases

XX  
XX Sequence 345 AA;  
SQ

Query Match 100.0%; Score 1848; DB 3; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.8e-181;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSLAGRTGTRASNLSSKQLSSDKQNGVDPRRERVTTISGNSIHS 60  
1 MLLIGLLLTSLAGRTGTRASNLSSKQLSSDKQNGVDPRRERVTTISGNSIHS 60  
DB 1 MLLIGLLLTSLAGRTGTRASNLSSKQLSSDKQNGVDPRRERVTTISGNSIHS 60

QY 61 PKPHTYPRNMVLTWRLVAVDENVRQLTFDERFGLEDDEDDICKDFVEVEPSDGSVL 120  
61 PKPHTYPRNMVLTWRLVAVDENVRQLTFDERFGLEDDEDDICKDFVEVEPSDGSVL 120  
DB 61 PKPHTYPRNMVLTWRLVAVDENVRQLTFDERFGLEDDEDDICKDFVEVEPSDGSVL 120

QY 121 GRWCGSGTVPGKQTSKGNHRIKRVSDSEYFSPGFCIHYSITMPVTTETSPSVLPSS 180  
121 GRWCGSGTVPGKQTSKGNHRIKRVSDSEYFSPGFCIHYSITMPVTTETSPSVLPSS 180  
DB 121 GRWCGSGTVPGKQTSKGNHRIKRVSDSEYFSPGFCIHYSITMPVTTETSPSVLPSS 180

QY 181 LSLDLNNNAVTAFTSTLEELIRYLEPRWQVLDLSLYKPTWQLGKAFLYGKSKVNLNL 240  
181 LSLDLNNNAVTAFTSTLEELIRYLEPRWQVLDLSLYKPTWQLGKAFLYGKSKVNLNL 240  
DB 181 LSLDLNNNAVTAFTSTLEELIRYLEPRWQVLDLSLYKPTWQLGKAFLYGKSKVNLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLANECQCVPK 300  
241 LKEEVKLYSCTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLANECQCVPK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLANECQCVPK 300

QY 301 VTKKYEHLQLRPKTVGKGLKSLTDVALHEHEECDCVCRGNAGG 345  
301 VTKKYEHLQLRPKTVGKGLKSLTDVALHEHEECDCVCRGNAGG 345



Db 301 VTKKYHEVLQLRPKTVGKGLHKSILTDVALBHHBECDCVCRGNAG 345

RESULT 3  
AAB48658  
ID AAB48658 standard; protein; 345 AA.

XX  
AC AAB48658;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Mouse zvegf3, SEQ ID NO:35.  
XX  
KM Mouse; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;  
KM murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;  
KM neovascularization; tissue repair; proliferation; differentiation;  
KM liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;  
KM periodontal disease; bone fracture; wound healing; vulnery; ischaemia;  
KM immunomodulation; hepatic.

XX  
OS Mus musculus.  
XX  
PN WO20006736-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 03-MAY-2000; 2000WO-US040047.  
XX  
PR 03-MAY-1999; 99US-00304216.  
PR 10-NOV-1999; 99US-0164463P.  
PR 04-FEB-2000; 2000US-0180169P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
XX  
DR WPI; 2000-687541/67.  
DR N-PSDB; AAC81583.  
XX  
PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
PT Alzheimer's disease.

XX  
PS Disclosure; Page 130-131; 143pp; English.

XX  
CC The invention relates to the human growth factor homologue zvegf4  
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member  
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654)  
CC characterised by a PDGF cysteine knot structure, and a CUB domain  
CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like  
CC activity, having mitogenic activity on fibroblasts, vascular smooth  
CC muscle cells and pericytes, and has also been shown to stimulate bone  
CC growth. The invention also relates to fusion proteins comprising human  
CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3  
CC fusions; expression constructs and host cells comprising human zvegf4  
CC nucleic acids; the recombinant expression of human zvegf4; an antibody  
CC which binds to human zvegf4 or a fragment thereof; a method of activating  
CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method  
CC of modulating the proliferation, differentiation, migration or metabolism  
CC of bone cells, comprising exposing bone cells to zvegf4-derived  
CC polypeptides; and a method of detecting a genetic abnormality in the  
CC zvegf4 gene of a patient. Zvegf4 proteins and derived fragments may be  
CC used to stimulate tissue development or repair, or cellular  
CC differentiation or proliferation. They are particularly used for the  
CC treatment or repair of liver damage, and may also be used to modulate  
CC neurite growth (e.g., in the treatment of Alzheimer's disease or multiple  
CC sclerosis). Due to their osteogenic activity, they may be used in the  
CC treatment of periodontal disease and fractures. They may also be used to  
CC enhance expansion and mobilisation of haematopoietic stem cells and  
CC endothelial precursor stem cells, which may be useful in the treatment of  
CC ischaemia, in wound healing, and in the modulation of the immune system.  
CC The present sequence represents mouse zvegf3

XX  
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 3; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1,8e-181;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTLGLLLTSALAGRTGRABSNLSKQLQSDSKQNGVQDRHRVVTISNGSITHS 60  
DB 1 MLTLGLLLTSALAGRTGRABSNLSKQLQSDSKQNGVQDRHRVVTISNGSITHS 60  
QY 61 PKFPHYPRMNVLMVRVAADENVRQLTFDERGLEDPEDDCKYDFVEVEBPSDSVL 120  
DB 61 PKFPHYPRMNVLMVRVAADENVRQLTFDERGLEDPEDDCKYDFVEVEBPSDSVL 120  
QY 121 GRWCGSGTVPGKQTSKNNHRIREFVSDEYPPSEPGFCIHYSIIMPQVETTPSPVLPSS 180  
DB 121 GRWCGSGTVPGKQTSKNNHRIREFVSDEYPPSEPGFCIHYSIIMPQVETTPSPVLPSS 180  
QY 181 LSLDLNNNAVTAFTSELRYLEPDRNOVDLSLYPTQOLGKAFLYGKKSRYVNLNL 240  
DB 181 LSLDLNNNAVTAFTSELRYLEPDRNOVDLSLYPTQOLGKAFLYGKKSRYVNLNL 240  
QY 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIFWPGCLVYKRCGNCACCLHNCQCVPYRK 300  
DB 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIFWPGCLVYKRCGNCACCLHNCQCVPYRK 300  
QY 301 VTKKYHEVLQLRPKTVGKGLHKSILTDVALBHHBECDCVCRGNAG 345  
DB 301 VTKKYHEVLQLRPKTVGKGLHKSILTDVALBHHBECDCVCRGNAG 345

RESULT 4  
AAE00998  
ID AAE00998 standard; protein; 345 AA.

XX  
AC AAE00998;  
XX  
DT 04-JUL-2001 (first entry)  
XX  
DE Mouse zvegf3 protein.  
XX  
KM Mouse; zvegf3 antagonist; cell proliferation; stellate cell activation;  
KM extracellular matrix production; fibrosis; VEGF-R; PDGF-C;  
KM platelet-derived growth factor; PDGF; vascular endothelial growth factor;  
KM VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;  
KM chronic active hepatitis; fulminant viral hepatitis; amyloidosis;  
KM diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;  
KM asbestosis; renal arteriosclerosis; post necrotic cirrhosis;  
KM diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;  
KM pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;  
KM bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;  
KM fibroproliferative disorder.

XX  
OS Mus musculus.  
XX  
PN WO200128586-A1.  
XX  
PD 26-APR-2001.  
XX  
PF 23-OCT-2000; 2000WO-US029270.  
XX  
PR 21-OCT-1999; 99US-0161653P.  
PR 12-NOV-1999; 99US-0165255P.  
PR 01-AUG-2000; 2000US-0222233P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Gilbertson DG;  
XX  
DR WPI; 2001-300278/31.  
DR N-PSDB; AAD04650.

PT Use of zvegf3 antagonist for reducing fibroproliferative disorder of  
PT kidney, liver and bone, reducing extracellular matrix production,  
PT creating fibrosis or reducing stellate cell activation in mammal.  
XX  
XX Example 2; Fig 2; 70pp; English.  
XX  
CC The patent discloses materials and methods for reducing cell  
CC proliferation or extracellular matrix production, treating fibrosis and  
CC reducing stellate cell activation in a mammal. The method comprises  
CC administering a composition containing a Zvegf3 antagonist in combination  
CC with a delivery vehicle. The Zvegf3 is a protein that is structurally  
CC related to platelet-derived growth factor (PDGF) and the vascular  
CC endothelial growth factors (VEGF). The Zvegf3 protein is also designated  
CC as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the  
CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat  
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active  
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1  
CC antitrypsin deficiency, fibrotic disorders of the kidney such as  
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic  
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders  
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,  
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,  
CC fibrotic disorders of pancreas, fibroproliferative disorders of the  
CC vasculature such as transplant vasculopathy and fibroproliferative  
CC disorders of the bone such as osteopetrosis and hyperostosis. The present  
CC sequence is mouse Zvegf3 protein  
XX  
XX  
SQ Sequence 345 AA;  
Query Match 100.0%; Score 1848; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.8e-181;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLTLTALAGORTGRASNLSSKQLSDSKONQVOPRHRVVTIGNSIHS 60  
DB 1 MLLGLLTLTALAGORTGRASNLSSKQLSDSKONQVOPRHRVVTIGNSIHS 60  
QY 61 PKRPHYPRNMVLMRLVAVDENVRQLTFDERFGLEDPEDDICXDFVVEEPPSDGSYL 120  
DB 61 PKRPHYPRNMVLMRLVAVDENVRQLTFDERFGLEDPEDDICXDFVVEEPPSDGSYL 120  
QY 121 GRMGSGCTVPKQKTSKGNHRIKRVSDYRPPSEPGFCHYSITMPQVETTSFVLPSS 180  
DB 121 GRMGSGCTVPKQKTSKGNHRIKRVSDYRPPSEPGFCHYSITMPQVETTSFVLPSS 180  
QY 181 LSLDLNNATATSTBELIRYLEPDRQVLDLSVYPTQLGKAFVYKSKVNNL 240  
DB 181 LSLDLNNATATSTBELIRYLEPDRQVLDLSVYPTQLGKAFVYKSKVNNL 240  
QY 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIFWPGCLVYKRCGACCLAHNCNECQCVPK 300  
DB 241 LKEEVKLYSCTPRNFVSIRBELKRTDTIFWPGCLVYKRCGACCLAHNCNECQCVPK 300  
QY 301 VTKKHEVLOLRPKTYGKGLKSLTDVALHHEBCDVCNGNAG 345  
DB 301 VTKKHEVLOLRPKTYGKGLKSLTDVALHHEBCDVCNGNAG 345  
RESULT 5  
ABG92894 standard; protein; 345 AA.  
XX  
AC ABG92894;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Mouse VEGF-like protein zvegf 3.  
XX  
KM VEGF; vascular endothelial growth factor; zvegf 3; mouse; chromosome 3;  
KM cell proliferation; differentiation; metabolism; migration;  
KM revascularization; solid tumour; diabetic retinopathy; psoriasis;  
KM rheumatoid arthritis; cancer; autoimmune disease; inflammation;  
KM myocardial ischaemia; scleroderma; fibrosis; glomerulosclerosis;

KW atherosclerosis; skin wound; ulcer; burn; skin grafting;  
KW female reproductive tract disorder; chronic liver disease;  
KW circulatory disorder; heart failure; neurodegenerative disease;  
KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;  
KW neurite outgrowth.  
XX  
XX Mus musculus.  
XX  
OS US6432673-B1.  
XX  
PN 13-ANG-2002.  
XX  
PD 07-DEC-1999; 99US-00457066.  
XX  
PF 07-DEC-1999; 98US-0111173P.  
XX  
PR 06-JUL-1999; 99US-0142576P.  
XX  
PR 21-OCT-1999; 99US-0161653P.  
XX  
PR 12-NOV-1999; 99US-0165255P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;  
PI Gilbertson DG, West JW;  
XX  
DR MPI; 2002-689759/74.  
XX  
DR N-PSDB; ABS68648.  
XX  
PT Novel polypeptide, designated zvegf3 useful for treating skin wounds,  
PT ulcers, burns, skin grafting, female reproductive tract disorders,  
PT Parkinson's disease, and Alzheimer's disease.  
XX  
XX Example 4; Fig 2; 68pp; English.  
XX  
XX The invention relates to an isolated polypeptide, designated zvegf3 (a  
XX vascular endothelial growth factor-like protein) of 11-136 amino acid  
XX residues in length and comprises the sequence appearing as ABG92894 from  
XX amino acid residues 235-345. Also included are an isolated protein  
XX comprising a first polypeptide disulphide bonded to a second polypeptide,  
XX where each of the first and second polypeptides is from zvegf 3, and  
XX where the protein modulates cell proliferation, differentiation,  
XX metabolism or migration, the zvegf 3 encoding polynucleotides and zvegf 3  
XX expression vectors and host cells. Zvegf 3 is useful as additives in  
XX tissue adhesives for promoting revascularisation of the healing tissue,  
XX for designing molecules that antagonise semaphorin-stimulated activities,  
XX including neurite growth, cardiovascular development, cartilage and limb  
XX development, and T and B-cell function, and for imaging tumours or other  
XX sites of abnormal cell proliferation and in gene therapy applications.  
XX The proteins are useful therapeutically to stimulate tissue development  
XX or repair, or cellular differentiation or proliferation, for stimulating  
XX the growth of fibroblast or smooth muscle cells, as molecular weight  
XX standards, as reagents in assays for determining circulatory level of the  
XX protein or as standards in the analysis of cell phenotype, for  
XX identifying inhibitors of their activity which are useful for reducing  
XX the growth of solid tumours; for treating diabetic retinopathy,  
XX psoriasis, rheumatoid arthritis, various forms of cancers, autoimmune  
XX disease, inflammation, myocardial ischaemia, scleroderma, and reducing  
XX fibrosis, including scar formation, keloids, liver fibrosis, lung  
XX fibrosis (e.g. silicosis, asbestosis), kidney fibrosis (including  
XX diabetic nephropathy), glomerulosclerosis, atherosclerosis, skin wounds,  
XX ulcers, burns, skin grafting, and female reproductive tract disorders,  
XX chronic liver disease (hepatitis), cirrhosis, Reye's syndrome, Wilson's  
XX disease, circulatory disorders e.g. heart failure, hepatic or portal vein  
XX thrombosis, cardiac sclerosis, neurodegenerative diseases such as  
XX multiple sclerosis, Parkinson's disease, Alzheimer's disease, and for  
XX regenerating neurite outgrowth following strokes. The gene for mouse  
XX zvegf3 is located on chromosome 3. The present sequence represents zvegf  
XX 3  
XX  
SQ Sequence 345 AA;  
Query Match 100.0%; Score 1848; DB 5; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.8e-181;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MLLIGLLLTSLAGORTGTRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60  
 1 MLLIGLLLTSLAGORTGTRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60  
 Db 1 MLLIGLLLTSLAGORTGTRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60  
 Qy 61 PKPHTYPRMMVLMVRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEVEPSDGSVL 120  
 61 PKPHTYPRMMVLMVRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEVEPSDGSVL 120  
 Db 61 PKPHTYPRMMVLMVRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEVEPSDGSVL 120  
 Qy 121 GRMGSGTVGKQTSKGNHRIIRFVSDPEYFSPGFCIHYSIIMPQVETSTSPSVLPSS 180  
 121 GRMGSGTVGKQTSKGNHRIIRFVSDPEYFSPGFCIHYSIIMPQVETSTSPSVLPSS 180  
 Db 121 GRMGSGTVGKQTSKGNHRIIRFVSDPEYFSPGFCIHYSIIMPQVETSTSPSVLPSS 180  
 Qy 181 LSLDLNNAVTAFTSTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240  
 181 LSLDLNNAVTAFTSTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240  
 Db 181 LSLDLNNAVTAFTSTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240  
 Qy 241 LKEEVKLYSCTPRNFVSIREELKRTDTITFWPGCLVYKRCGNCACCLHNCNCCQVPRK 300  
 241 LKEEVKLYSCTPRNFVSIREELKRTDTITFWPGCLVYKRCGNCACCLHNCNCCQVPRK 300  
 Db 241 LKEEVKLYSCTPRNFVSIREELKRTDTITFWPGCLVYKRCGNCACCLHNCNCCQVPRK 300  
 Qy 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345  
 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345  
 Db 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345

RESULT 6  
 AAE13213  
 ID AAE13213 standard; protein; 345 AA.  
 AC AAE13213;  
 XX 12-FEB-2002 (first entry)  
 DT Mouse platelet-derived growth factor (PDGF-C) protein.  
 DE Mouse; transgenic animal; platelet derived growth factor C; PDGF-C;  
 KM cardiac hypertrophy; fibrosis.  
 XX Mus sp.  
 OS WO200172132-A1.  
 PN 04-OCT-2001.  
 PD 28-MAR-2001; 2001WO-US009855.  
 PF 28-MAR-2000; 2000US-0192507P.  
 PR 28-MAR-2000; 2000US-0192507P.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Eriksson U, Li X, Ponten A, Aase K, Li H;  
 PI WPI; 2002-010706/01.  
 DR A transgenic animal over-expressing platelet derived growth factor C is  
 PT useful to study and find therapy for disease associated with PDGF-C over-  
 PT expression, including cardiac hypertrophy and fibrosis.  
 XX Example 4; Page 42-43; 48pp; English.  
 PS The patent discloses a method for producing a transgenic, non-human  
 CC animal over-expressing a platelet derived growth factor C (PDGF-C), or  
 CC its functional fragment or analogue. The method involves introducing a  
 CC transgenic PDGF-C DNA into a cell of a non-human animal, introducing the  
 CC cell into a non-human animal and allowing the cell to develop into a  
 CC transgenic, non-human animal. The transgenic animal is useful as a model  
 CC to study disease states characterised by over-expression of PDGF-C and to  
 CC find therapy for those diseases, particularly hypertrophy and fibrosis in  
 CC various organs including the heart. The present sequence is PDGF-C  
 CC protein from mouse  
 XX Sequence 345 AA;  
 SQ

Query Match 100.0%; Score 1848; DB 5; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-181;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MLLIGLLLTSLAGORTGTRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60  
 1 MLLIGLLLTSLAGORTGTRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60  
 Db 1 MLLIGLLLTSLAGORTGTRAESNLSSKQLSSDKQNGVDPRHRRVTTISGNGSIHS 60  
 Qy 61 PKPHTYPRMMVLMVRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEVEPSDGSVL 120  
 61 PKPHTYPRMMVLMVRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEVEPSDGSVL 120  
 Db 61 PKPHTYPRMMVLMVRLVAVDENVRIOLTDERFGLEDPEDDICKYDFVEVEPSDGSVL 120  
 Qy 121 GRMGSGTVGKQTSKGNHRIIRFVSDPEYFSPGFCIHYSIIMPQVETSTSPSVLPSS 180  
 121 GRMGSGTVGKQTSKGNHRIIRFVSDPEYFSPGFCIHYSIIMPQVETSTSPSVLPSS 180  
 Db 121 GRMGSGTVGKQTSKGNHRIIRFVSDPEYFSPGFCIHYSIIMPQVETSTSPSVLPSS 180  
 Qy 181 LSLDLNNAVTAFTSTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240  
 181 LSLDLNNAVTAFTSTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240  
 Db 181 LSLDLNNAVTAFTSTLEELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKRVNLNL 240  
 Qy 241 LKEEVKLYSCTPRNFVSIREELKRTDTITFWPGCLVYKRCGNCACCLHNCNCCQVPRK 300  
 241 LKEEVKLYSCTPRNFVSIREELKRTDTITFWPGCLVYKRCGNCACCLHNCNCCQVPRK 300  
 Db 241 LKEEVKLYSCTPRNFVSIREELKRTDTITFWPGCLVYKRCGNCACCLHNCNCCQVPRK 300  
 Qy 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345  
 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345  
 Db 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALHEHRECDVCVCRGNAG 345

RESULT 7  
 AAB47890  
 ID AAB47890 standard; protein; 345 AA.  
 AC AAB47890;  
 XX 16-MAY-2002 (first entry)  
 DT Mouse zvegf3.  
 DE Human; mouse; zvegf3; zvegf4; platelet derived growth factor; PDGF;  
 KM homolog; growth; bone; ligament; cartilage; proliferation; osteoblast;  
 KM chondrocyte; bony defect; fracture; bone graft; implant;  
 KM periodontal pocket; osteoclast; bone marrow stem cell; osteoporosis.  
 XX Mus musculus.  
 OS US200204225-A1.  
 PN 10-JAN-2002.  
 PD 29-MAR-2001; 2001US-00823033.  
 PF 07-DEC-1998; 98US-0111173P.  
 PR 06-JUL-1999; 99US-0142576P.  
 PR 21-OCT-1999; 99US-0161653P.  
 PR 12-NOV-1999; 99US-0165255P.  
 PR 07-DEC-1999; 99US-00457066.  
 PR 31-MAR-2000; 2000US-0193723P.  
 XX (HART/) HART C E.  
 PA (GILB/) GILBERTSON D G.  
 PI Hart CE, Gilbertson DG;  
 XX WPI; 2002-171026/22.  
 DR N-PSDB; AAI72444.  
 DR Promoting growth of bone, ligament or cartilage in a mammal, involves  
 XX administering to the mammal a protein which comprises growth factor  
 PT domain of zvegf3 protein, a homolog of platelet-derived growth factor.  
 XX Claim 1; Page 19-20; 31pp; English.  
 PS

XX The sequences given in ABA71889-90 represent human and mouse zvegf3,  
 CC respectively. zvegf3 is a platelet derived growth factor (PDGF) homolog  
 CC and it was used in the method of the invention for promoting growth of  
 CC bone, ligament or cartilage and stimulating proliferation of osteoblasts  
 CC or chondrocytes in a mammal. The proteins used were preferably a dimeric  
 CC protein of residues 235-345 of human zvegf3 or all of the mouse zvegf3  
 CC protein, with a delivery vehicle. The method of the invention is useful  
 CC for promoting growth of bone, ligament or cartilage in a mammal, where  
 CC the composition is administered at a site of a bony defect, preferably a  
 CC fracture, bone graft site, implant site, or periodontal pocket, and for  
 CC stimulating proliferation of osteoblasts or chondrocytes in a mammal. It  
 CC is further useful for promoting proliferation of osteoblasts,  
 CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone  
 CC marrow stem cells are harvested from a patient prior to culture. The  
 CC method is therefore useful for treating osteoporosis

XX  
 SO Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 5; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-181;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAAGRTGTRASNSLSKQLSSDKQNGVODPRHRRVTTISGNGSIHS 60  
 DB 1 MLLGLLLTSLAAGRTGTRASNSLSKQLSSDKQNGVODPRHRRVTTISGNGSIHS 60  
 QY PKPHTYPRMVLVRLVAVDENVRILQTFDERFGLEDPEDDICKYDFEVEBPSDGSYL 120  
 DB 61 PKPHTYPRMVLVRLVAVDENVRILQTFDERFGLEDPEDDICKYDFEVEBPSDGSYL 120  
 QY 121 GRWCGSGTVPGKQTSKGNHRIKRVSDPEPSPGFCIHYSIIMPQVETTTSPSVLPSS 180  
 DB 121 GRWCGSGTVPGKQTSKGNHRIKRVSDPEPSPGFCIHYSIIMPQVETTTSPSVLPSS 180  
 QY 181 LSLDLNNATVAFSTLEELIRLEPRMVDLSLYKPTWOLGKAPLYGKKSKVNNL 240  
 DB 181 LSLDLNNATVAFSTLEELIRLEPRMVDLSLYKPTWOLGKAPLYGKKSKVNNL 240  
 QY 241 LKEEVLVSTCTPRNFSVSIREELEKRTDTTFMFGCLLVKRCGNCACCLHNCNCCQVPRK 300  
 DB 241 LKEEVLVSTCTPRNFSVSIREELEKRTDTTFMFGCLLVKRCGNCACCLHNCNCCQVPRK 300  
 QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAGG 345  
 DB 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAGG 345

RESULT 8  
 ID ABA72435 standard; protein; 345 AA.  
 XX  
 AC ABA72435;  
 XX  
 DT 16-JUN-2003 (first entry)  
 XX  
 DE Mouse ZVEGF4-related protein #1.  
 XX  
 KW Growth factor homologue; ZVEGF4; proliferation; differentiation;  
 KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;  
 KW neurite growth; cardiovascular development; limb development;  
 KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;  
 KW autoimmune disease; inflammation; retinopathy; haemangioma;  
 KW ischemic event; neuropathy; acute nerve damage; stroke;  
 KW central nervous system disease; peripheral nervous system disease.

XX  
 OS Mus musculus.  
 OS  
 XX US6495668-B1.  
 XX  
 XX  
 PD 17-DEC-2002.  
 XX  
 PF 03-MAY-2000; 2000US-00564595.

XX  
 PR 03-MAY-1999; 99US-0132250P.  
 PR 10-NOV-1999; 99US-0164463P.  
 PR 04-FEB-2000; 2000US-0180169P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Gilbert T, Hart CE, Shepard PO, Gilbertson DG;  
 XX  
 DR WPI: 2003-352153/33.  
 DR N-PSDB; ACA64117.  
 XX  
 PT Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical  
 PT composition as, e.g. therapeutic agents, diagnostic agents, and research  
 PT tools and reagents, includes polypeptides from amino acid residues.  
 XX  
 PS Disclosure; Col 95-98; 67pp; English.

XX  
 CC The invention relates to an isolated protein comprising a first  
 CC polypeptide disulphide-bonded to a second polypeptide. The first and  
 CC second polypeptides are from 113-138 amino acid residues and comprises  
 CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The  
 CC protein stimulates proliferation, differentiation, or migration of  
 CC mesenchymal cells and may modulate activities mediated by cell surface  
 CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-  
 CC semaphorin interactions which may be of use in neurite growth,  
 CC cardiovascular development, cartilage and limb development, T- and B-cell  
 CC functions as well as treating rheumatoid arthritis, various forms of  
 CC cancer, autoimmune diseases, inflammation, retinopathies, haemangomas,  
 CC ischemic events, neuropathies, acute nerve damage, central nervous  
 CC system diseases and peripheral nervous system diseases including stroke.  
 CC The isolated protein is also used for a pharmaceutical composition as  
 CC therapeutic agents, diagnostic agents, and research tools and reagents.  
 CC It can be used in the study and regulation of cell and tissue  
 CC development, as components of cell culture media. The proteins can form  
 CC homodimers or heterodimers that act on tissues to control organ  
 CC development by modulating cell proliferation, migration, differentiation,  
 CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3  
 CC -23.1. A transgene construct was made for producing mice transgenic for  
 CC human ZVEGF4. The construct contained human growth hormone gene control  
 CC regions. The present sequence is a ZVEGF4-related protein sequence. Note:  
 CC The present sequence is included in the sequence listing but is not  
 CC mention elsewhere in the specification

XX  
 SO Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 6; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-181;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAAGRTGTRASNSLSKQLSSDKQNGVODPRHRRVTTISGNGSIHS 60  
 DB 1 MLLGLLLTSLAAGRTGTRASNSLSKQLSSDKQNGVODPRHRRVTTISGNGSIHS 60  
 QY 61 PKPHTYPRMVLVRLVAVDENVRILQTFDERFGLEDPEDDICKYDFEVEBPSDGSYL 120  
 DB 61 PKPHTYPRMVLVRLVAVDENVRILQTFDERFGLEDPEDDICKYDFEVEBPSDGSYL 120  
 QY 121 GRWCGSGTVPGKQTSKGNHRIKRVSDPEPSPGFCIHYSIIMPQVETTTSPSVLPSS 180  
 DB 121 GRWCGSGTVPGKQTSKGNHRIKRVSDPEPSPGFCIHYSIIMPQVETTTSPSVLPSS 180  
 QY 181 LSLDLNNATVAFSTLEELIRLEPRMVDLSLYKPTWOLGKAPLYGKKSKVNNL 240  
 DB 181 LSLDLNNATVAFSTLEELIRLEPRMVDLSLYKPTWOLGKAPLYGKKSKVNNL 240  
 QY 241 LKEEVLVSTCTPRNFSVSIREELEKRTDTTFMFGCLLVKRCGNCACCLHNCNCCQVPRK 300  
 DB 241 LKEEVLVSTCTPRNFSVSIREELEKRTDTTFMFGCLLVKRCGNCACCLHNCNCCQVPRK 300  
 QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAGG 345  
 DB 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALHHEECDCVCRGNAGG 345

RESULT 9  
 ABG76398  
 ID ABG76398 standard; protein, 345 AA.  
 XX  
 AC ABG76398;  
 XX  
 DT 22-MAY-2003 (first entry)  
 XX  
 DE Mouse growth factor homologue, zvegf3.  
 XX  
 KM Mouse; growth factor homologue; zvegf3; fibroblast; smooth muscle cell;  
 KM full-thickness platelet-derived growth factor alpha receptor; PDGF;  
 KM prolonged bleeding; periodontal disease; tissue adhesive; liver damage;  
 KM revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;  
 KM chronic active hepatitis; hepatic chronic passive congestion; stroke;  
 KM central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;  
 KM portal vein thrombosis; cardiac sclerosis; new vessel formation;  
 KM endothelial precursor stem cell; neovascularisation; wound healing;  
 KM organ transplant; tissue grafting; peripheral neuropathy; spinal cord;  
 KM sensory neurite outgrowth; brain damage; head injury; paralysis;  
 KM spinal injury; neurodegenerative disease; diabetic retinopathy;  
 KM psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;  
 KM lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;  
 KM proliferative vascular disorder; ocular neovascularisation;  
 KM inflammatory disorder; rheumatoid arthritis; vasculogenesis;  
 KM angiogenesis; nervous system disorder; cytostatic; hepatotropic;  
 KM vulnery; tranquilliser; cerebroprotective; neuroprotective; nootropic;  
 KM ophthalmological; dermatological; coagulant; cardiant.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2002177193-A1.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 02-MAY-2002; 2002US-00139583.  
 XX  
 PR 07-DEC-1998; 98US-0111173P.  
 PR 06-JUL-1999; 99US-0142576P.  
 PR 21-OCT-1999; 99US-0161653P.  
 PR 12-NOV-1999; 99US-0165255P.  
 PR 07-DEC-1999; 99US-00457066.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 PI Gao Z, Hart CE, Piddington CS, Shepard PO, Shoemaker KB;  
 PI Gilbertson DG, West JW;  
 XX  
 DR WPI; 2003-328485/31.  
 DR N-PSDB; ABX93182.  
 XX  
 PT New isolated zvegf3 polypeptide, useful for treating cancer, Alzheimer's  
 PT disease, Parkinson's disease, chronic active hepatitis, hepatic vein  
 PT thrombosis, comprises growth factor domain and CUB domain.  
 XX  
 PS Claim 1; Fig 6; 73pp; English.  
 XX  
 CC The present invention relates to the isolation of a growth factor  
 CC homologue referred to as zvegf3, and the polynucleotide sequence encoding  
 CC it. The zvegf3 polypeptide is useful for stimulating the growth of  
 CC fibroblasts or smooth muscle cells, or for activating a cell-surface  
 CC platelet-derived growth factor (PDGF) alpha receptor. The zvegf3  
 CC polypeptide is useful as a PDGF alpha receptor agonist and thus is useful  
 CC for treating full-thickness skin wounds, female reproductive tract and  
 CC prolonged bleeding, periodontal disease, damaged liver tissue, and  
 CC duodenal ulcers. The polypeptide is also useful as an additive in tissue  
 CC adhesives for promoting revascularisation of healing tissue. The zvegf3  
 CC polypeptide is also useful for treating liver damage including damage due  
 CC to liver disease, chronic active hepatitis, hepatic chronic passive  
 CC congestion (CPC), central haemorrhagic necrosis (CHN), hepatic vein

thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of  
 CC cirrhosis. The polypeptide is useful for enhancing expansion and  
 CC mobilisation of endothelial precursor stem cells, creating and  
 CC stabilising new vessel formation in areas requiring neovascularisation,  
 CC including areas of ischaemia, organ transplants, wound healing, and  
 CC tissue grafting. It may be used for treating peripheral neuropathies by  
 CC increasing spinal cord and sensory neurite outgrowth, and as part of  
 CC therapeutic treatment for the regeneration of neurite outgrowths  
 CC following strokes, brain damage caused by head injuries, and paralysis  
 CC caused by spinal injuries. Application may also be made in treating  
 CC neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease,  
 CC Parkinson's disease), diabetic retinopathy, psoriasis, arthritis,  
 CC scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung  
 CC fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds  
 CC zvegf3 is useful for blocking the mitogenic, chemotactic, or angiogenic  
 CC effects of zvegf3, and for treating proliferative vascular disorders,  
 CC ocular neovascularisation, inflammatory disorders, rheumatoid arthritis,  
 CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,  
 CC and diseases of the nervous system. The present sequence represents mouse  
 CC zvegf3  
 XX  
 SQ Sequence 345 AA;  
 XX  
 Query Match 100.0%; Score 1848; DB 6; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 1,8e-181;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLILGILLITSLAAGRTGTRAESNLSSKQLQSDKEQNGVQDPRHRRVVTISGNGSIHS 60  
 DB 1 MLILGILLITSLAAGRTGTRAESNLSSKQLQSDKEQNGVQDPRHRRVVTISGNGSIHS 60  
 QY 61 PKPHTYPRMVLVWRVVADEVNRVQLTDERRGLEDPPDDICXQFVVEEPPSDSVL 120  
 DB 61 PKPHTYPRMVLVWRVVADEVNRVQLTDERRGLEDPPDDICXQFVVEEPPSDSVL 120  
 QY 121 GRMGSGTVPGKOTSKGNHRIHFVSDYEPSEBGFCHYSIIMPQVETTSPEVLPPSS 180  
 DB 121 GRMGSGTVPGKOTSKGNHRIHFVSDYEPSEBGFCHYSIIMPQVETTSPEVLPPSS 180  
 QY 181 LSLDLNNAVTAFTSEELIRYLEPDRQVLDLSYKPTMQLGKAFLYGKSKRVNLNL 240  
 DB 181 LSLDLNNAVTAFTSEELIRYLEPDRQVLDLSYKPTMQLGKAFLYGKSKRVNLNL 240  
 QY 241 LKEEVKLYSCTPRNFVSITBELKRTTITWPGCLVYKRGNCACCLHNCNEQCVPK 300  
 DB 241 LKEEVKLYSCTPRNFVSITBELKRTTITWPGCLVYKRGNCACCLHNCNEQCVPK 300  
 QY 301 VTKKYHEVLDLRPTGVKGLKSLTDVALHEHEBCDCVCRGNAGG 345  
 DB 301 VTKKYHEVLDLRPTGVKGLKSLTDVALHEHEBCDCVCRGNAGG 345  
 RESULT 10  
 AAY41766  
 ID AAY41766 standard; protein, 345 AA.  
 XX  
 AC AAY41766;  
 XX  
 DT 07-DEC-1999 (first entry)  
 XX  
 DE Human PRO200 protein sequence.  
 XX  
 KM Human; PRO, EST, expressed sequence tag; PCR primer; hybridisation;  
 KM probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KM secreted protein; transmembrane protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09946281-A2.  
 PN 16-SEP-1999.  
 PD 08-MAR-1999; 99MO-US005028.  
 XX

XX  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 22-MAR-1998; 98US-0079224P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 31-MAR-1998; 98US-0080105P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 09-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083332P.  
PR 29-APR-1998; 98US-0083382P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083544P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084416P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0085703P.  
PR 22-MAY-1998; 98US-0086322P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
XX  
XX WPI: 1999-551358/46.  
DR N-PSDB; AA234236.  
XX  
XX New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders.  
XX  
PS Claim 12; Fig 207; 530pp; English.  
XX  
XX The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of CC antisense sequences. They can also be used to create transgenic animals. CC The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to CC AA41774 represent polynucleotide and polypeptide sequence given in the CC exemplification of the present invention  
XX  
SQ Sequence 345 AA;  
Query Match 90.2%; Score 1667; DB 2; Length 345;  
Best Local Similarity 87.0%; Pred. No. 8, 6e-163;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSLAAGRTGTRAEISNLSKLTQSSDEKQGVDPHRRVVTISGNGSTIS 60  
DB 1 MSIFGLLLTSLAAGRTGTRAEISNLSKLTQSSDEKQGVDPHRRVVTISGNGSTIS 60  
QY 61 PRPHTYPRNMYLVNRLVAVDENVRITQLFEDRFGLEDEDDICXDFVEVEPSDGSYL 120  
DB 61 PRPHTYPRNMYLVNRLVAVDENVRITQLFEDRFGLEDEDDICXDFVEVEPSDGSYL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDXEPSPGFCIHYSITMPQVETTSPLYLPPSS 180  
DB 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDXEPSPGFCIHYSITMPQVETTSPLYLPPSS 180  
QY 122 GRWCGSGTVPGKQTSKGNHRIIRFVSDXEPSPGFCIHYSITMPQVETTSPLYLPPSS 180  
DB 122 GRWCGSGTVPGKQTSKGNHRIIRFVSDXEPSPGFCIHYSITMPQVETTSPLYLPPSS 180  
QY 181 LSLDLINNAVTFSTBELIRYLEPDRQVDDLSLYKPWQLLGAFLYGGKSKYVNL 240  
DB 181 LSLDLINNAVTFSTBELIRYLEPDRQVDDLSLYKPWQLLGAFLYGGKSKYVNL 240  
QY 241 LKEEVKLYSCPRNRSVSIIRBELKRTDTFMFGCLLVKRCGNACCLHNGECOCVPRK 300  
DB 241 LKEEVKLYSCPRNRSVSIIRBELKRTDTFMFGCLLVKRCGNACCLHNGECOCVPRK 300  
QY 301 VTKKHEVQLRPKTGKGLHSLTDVALHHEECDCVCRGNAGG 345  
DB 301 VTKKHEVQLRPKTGKGLHSLTDVALHHEECDCVCRGNAGG 345  
RESULT 11

AA30023  
ID AAY30023 standard; protein; 345 AA.  
AC AAY30023;  
XX  
XX  
XX 11-OCT-1999 (first entry)  
DT  
XX Human vascular endothelial growth factor related protein.  
DE  
XX Vascular endothelial growth factor related protein; VEGF-R protein;  
KW tissue growth inhibition; tumour growth; cancer; tissue growth;  
KW angiogenesis; coronary artery blockage.  
XX  
XX Homo sapiens.  
OS  
XX MO9937671-A1.  
PN  
XX 29-JUL-1999.  
PD  
XX 26-JAN-1999; 99WO-US001574.  
PF  
XX 27-JAN-1998; 98US-0072635P.  
PR 05-JUN-1998; 98US-0086089P.  
PR 24-JUN-1998; 98US-0090544P.  
PR 31-AUG-1998; 98US-0098548P.  
XX  
XX (ELIL ) LILLY & CO ELI.  
PA  
XX Dou S, Na S, Song HY;  
PI  
XX WPI; 1999-458680/38.  
DR N-PSDB; AAX86352.  
XX  
XX A vascular endothelial growth factor related protein and related  
PT polynucleotide, useful for identifying antagonists and binding compounds.  
XX  
XX Claim 1; Page 56-58; 62pp; English.  
XX  
XX The present sequence represents a vascular endothelial growth factor  
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify  
CC compounds that bind to it or that antagonize its activity. VEGF-R  
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting  
CC tissue growth. This is useful for inhibiting tumour growth and for  
CC treating cancer. VEGF-R itself can be used to stimulate tissue growth,  
CC angiogenesis and to treat coronary artery blockage. The VEGF-R coding  
CC sequence can be used for the recombinant production of the VEGF-R protein  
XX  
XX Sequence 345 AA;  
SQ  
Query Match 90.2%; Score 1667; DB 2; Length 345;  
Best local Similarity 87.0%; Pred. No. 8,6e-163;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLIGLLLTSLALAGORTGTRAESNLSSKQLSDPKENGQVQDPHREVTITSGNGSIHS 60  
Db 1 MSILGILLTSLALAGORTGTRAESNLSSKQLSDPKENGQVQDPHREVTITSGNGSIHS 60  
QY 61 PKPHTYPRNVLVRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEEPPSGSVL 120  
Db 61 PRPHTYPRNVLVRLVAVDENVRILQTFDERFGLDEPDICKYDFVEVEEPPSGSVL 120  
QY 121 GRMGSGTVPGKQSKGNQIRIFVSDYFPSEPEFCIHYNIMVQFTFAVSPVLPPSA 180  
Db 121 GRMGSGTVPGKQSKGNQIRIFVSDYFPSEPEFCIHYNIMVQFTFAVSPVLPPSA 180  
QY 181 LSLDLLANNAVAFSTLEELIRYLEPDRMQVDLSLYKFTWOLGKAPLYGKSKYVNLT 240  
Db 181 LPDLIDNNAITAFSTLEELIRYLEPDRMQVDLSLYKFTWOLGKAPLYGKSKRYVDLT 240  
QY 241 LKEEYKLYSCTPRNFSVIREBLKRTDTIIFWPGCLLVRCGNCACCLAHNCEQCVPRK 300  
Db 241 LTEEYKLYSCTPRNFSVIREBLKRTDTIIFWPGCLLVRCGNCACCLAHNCEQCVPRK 300

QY 301 VTKKYHEVLTQLRPKTVGKGLHKSJLTDVALBHEHECDVCVCRGNAG 345  
Db 301 VTKKYHEVLTQLRPKTVGKGLHKSJLTDVALBHEHECDVCVCRGNAG 345

RESULT 12  
AAY33679  
ID AAY33679 standard; protein; 345 AA.  
AC AAY33679;  
XX  
XX 11-JAN-2000 (first entry)  
DT  
XX Human VEGF-E protein.  
DE  
XX VEGF-E, human; vascular endothelial cell growth factor; wound repair;  
KW treatment; cardiovascular disorder; endothelial disorder; therapy;  
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
KW angiogenic disorder; age-related macular degeneration; vascular disease;  
KW neovascularization; tumor; gene mapping.  
XX  
XX Homo sapiens.  
OS  
XX MO9947677-A2.  
PN  
XX 23-SEP-1999.  
PD  
XX 10-MAR-1999; 99WO-US005190.  
PF  
XX 17-MAR-1998; 98US-00040220.  
PR 02-NOV-1998; 98US-00184216.  
XX  
XX (GERTH ) GENENTECH INC.  
PA  
XX Ferrara N, Kuo SS;  
PI  
XX WPI; 1999-580306/49.  
DR N-PSDB; AAZ23691.  
XX  
XX New growth factor polypeptide useful for treating cardiovascular or  
PT endothelial disorders, e.g. cardiac hypertrophy.  
XX  
XX Claim 1; Fig 2; 122pp; English.  
XX  
XX This invention describes the isolation of a novel human vascular  
CC endothelial cell growth factor-E (VEGF-E) polypeptide which has  
CC astringent, vulnery and cardiant activity. VEGF-E can be administered  
CC therapeutically, especially by expressing encoding polynucleotides, to  
CC treat cardiovascular or endothelial disorders in mammals, especially  
CC humans. It is useful in wound repair and tissue generation and  
CC regeneration, and may especially be used to treat cardiac hypertrophy. It  
CC can be combined with a carrier in pharmaceutical compositions, which can  
CC be administered to treat disorders as above. VEGF-E can be used to screen  
CC for antagonists and agonists, and the antagonists administered to treat  
CC angiogenic disorders in mammals (especially humans) e.g. cancer or age-  
CC related macular degeneration. It can be used to generate antibodies, as  
CC useful therapeutically as antagonists, as above. The antibodies are also  
CC useful to detect VEGF-E polypeptide, especially to diagnose  
CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.  
CC vascular disease, or neovascularization associated with tumor formation),  
CC by contacting the antibody with a tissue sample and detecting formation  
CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-  
CC E can be used to diagnose cardiovascular and endothelial disorders in  
CC mammals, by detecting abnormally high or low VEGF-E gene expression in  
CC tissue samples. They can also be used to diagnose a disease or  
CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a  
CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by  
CC detecting a mutation in the VEGF-E encoding sequence isolated from a  
CC sample. They may also be used to produce probes useful to detect related  
CC sequences or for gene mapping. This sequence represents the human VEGF-E  
CC protein described in the method of the invention  
XX  
XX Sequence 345 AA;





```

Db      1 MSFLGILLTSALAGRGQTGAESNLSSKQFSSNKEQNGVDPQHRITITVSTNGSIHS 60
Qy      61 PKPHTTPRMVTLVWRLVAVDENRIQLTDERFGLEDPEDDICKYDFVEEESDGSVL 120
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Db      121 GRMGSGTVGKQSKGNQIRIRFVSDPEPSEBGFCHVNIWPOTEAVSPVLPSPA 180
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        241 LTBELVRLYSCTPRNFVSISIRELKRDTITFWPGCLLYKRCGNCACCLHNCNCCQVPSK 300
Qy      301 VTKKYHEVLOLRPTKGVGLHKSLLTDVALHHEBECDCVCRGNAGG 345
        301 VTKKYHEVLOLRPTKGVGLHKSLLTDVALHHEBECDCVCRGSTGG 345
Db
RESULT 14
AAB19578
ID      AAB19578 standard; protein; 345 AA.
XX
AC      AAB19578;
XX
DT      22-JAN-2001 (first entry)
XX
DE      Human PRO200 (vascular endothelial growth factor E).
XX
KW      PRO200; vascular epithelial growth factor E; VEGF-E; human;
KW      ocular disease; retinopathy; maculopathy; therapy; retinitis pigmentosa;
KW      macular degeneration; retinal detachment; retinal tear; macular hole;
KW      myopia; traumatic choriorretinopathy; acute retinal necrosis syndrome;
KW      contusion; edema; retinal vision occlusion; vascular disease;
KW      retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Peptide
        1..14
        /label= Signal_peptide
FT      Protein
        15..345
        /label= Mature_Pro200
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        15..21
        /note= "N-myristoylation"
FT      Modified-site
        25..29
        /note= "Asn is N-glycosylated"
FT      Modified-site
        55..59
        /note= "Asn is N-glycosylated"
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        117..123
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        /note= "N-myristoylation"
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FT      Modified-site
        281..287
        /note= "Asn is N-glycosylated"
FT      Modified-site
        282..288
        /note= "N-myristoylation"
FT      Modified-site
        319..325
        /note= "N-myristoylation"
FT      Modified-site
        /note= "Amidation"
XX
PN      WO200053760-A2.
XX
PD      14-SEP-2000.
XX
PF      10-MAR-2000; 2000WO-US006319.
XX
PR      12-MAR-1999; 99US-0123957P.

```

```

XX      (GERTH ) GENENTECH INC.
PA      Ferreira N, Goddard A, Gurney AL, Hebert C, Henzel MJ,
XX      Kabakoff RC, Klein RD, Kljavin IJ, Kuo SS, La Fleur M, Wood WI,
PI      WPI; 2000-587437/55.
DR      N-PSDB; AAB8515.
XX
PT      Novel PRO polypeptides useful for preventing or rescuing retinal cells
PT      from injury caused by ocular diseases such as retinitis pigmentosa,
PT      retinopathy, retinal degenerative diseases, degenerative myopia, uveitis.
PS      Claim 2; Fig 2; 140pp; English.
XX
CC      The present sequence is that of human PRO200 or vascular endothelial
CC      growth factor E (VEGF-E), as predicted from a cDNA clone (see AAB8515)
CC      that was isolated from a glioma cell line G61 library using probes (see
CC      AAB8523-26) based on an expressed sequence tag (see AAB8522) that
CC      showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a
CC      pI of about 6.06. A method for producing PRO polypeptides, including
CC      PRO200, using a host cell transformed with a vector comprising a PRO
CC      nucleic acid is claimed. The invention relates to the use of PRO
CC      polypeptides to delay, prevent or rescue retinal cells such as retinal
CC      neurons selected from photoreceptors, retinal ganglion cells, displaced
CC      retinal ganglion cells, amacrine cells, displaced amacrine cells,
CC      horizontal and bipolar neurons, and supportive cells (including Mueller
CC      cells and pigment epithelial cells) from injury and degradation. The
CC      retinal cells are preferably photoreceptors and photoreceptor cell injury
CC      or death is caused by retinal injury, light or environmental trauma or by
CC      an ocular disease selected from retinitis pigmentosa, macular
CC      degeneration, including age-related, retinal detachment, retinal tears,
CC      retinopathy, retinal degenerative diseases, macular holes, degenerative
CC      myopia, acute retinal necrosis syndrome, traumatic choriorretinopathies or
CC      contusion such as Purtscher's retinopathy, edema, ischemic conditions
CC      such as central or branch retinal vision occlusion, collagen vascular
CC      diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and
CC      occlusion associated with Fales disease and systemic lupus erythematosus
CC      (claimed)
XX
SQ      Sequence 345 AA;
XX
Query Match          90.2%; Score 1667; DB 3; Length 345;
Best Local Similarity 87.0%; Pred. No. 8.6e-153;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
Qy      1 MLILGILLTSALAGRGQTGAESNLSSKQLSDKEQNGVDPQHRITITVSTNGSIHS 60
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Qy      181 LSLDLNNAVTAFTLEBELRYLEPDRMQVDLSLYKPTQMLGKAFLYGKKSRVNLNL 240
        181 LPDLNNATTAFTLEBELRYLEPERMQVDLELYRPTQMLGKAFVFGKSRVNLNL 240
Db
Qy      241 LKEEVKLYSCTPRNFVSISIRELKRDTITFWPGCLLYKRCGNCACCLHNCNCCQVPRK 300
        241 LTBELVRLYSCTPRNFVSISIRELKRDTITFWPGCLLYKRCGNCACCLHNCNCCQVPSK 300
Db
Qy      301 VTKKYHEVLOLRPTKGVGLHKSLLTDVALHHEBECDCVCRGNAGG 345
        301 VTKKYHEVLOLRPTKGVGLHKSLLTDVALHHEBECDCVCRGSTGG 345
Db
RESULT 15
AAB10651

```

ID AAB10651 standard; protein; 345 AA.  
 AC AAB10651;  
 DT 19-JAN-2001 (first entry)  
 DE Human VEGF-X protein #3.  
 KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;  
 KW antiinflammatory; antiarthritic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth.  
 OS Homo sapiens.  
 PN W0200037641-A2.  
 PD 29-JUN-2000.  
 PF 21-DEC-1999; 99WO-US030503.  
 PR 22-DEC-1998; 98GB-00028377.  
 PR 18-MAR-1999; 99US-0124967P.  
 PR 08-NOV-1999; 99US-0164131P.  
 PA (JANC ) JANSSEN PHARM NV.  
 PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;  
 PI Dhanraj SN, Xu J;  
 DR WPI; 2000-442669/38.  
 PT New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds.  
 PS Claim 72; Fig 12; 127pp; English.  
 XX This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has  
 CC vulnerary, cytostatic, antiinflammatory, antidiabetic, antipsoriatic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the human VEGF-X protein  
 CC described in the method of the invention  
 XX  
 SQ Sequence 345 AA;

Query Match 90.2%; Score 1667; DB 3; Length 345;  
 Best Local Similarity 87.0%; Pred. No. 8.6e-163;  
 Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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 DB 61 PRPHYPRNMLVWRLVAVDENVRQLTFDERFGLEDPEDDICKYDFVEVEEPPDSGYL 120  
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DB 121 GRWCGGTVPGRKTSKGNHRIKRVFVSDYFSPGFCIHYSIMPOVETTSPTVPPSS 180  
 QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDDSLYKPTWOLLGKAFLYGKSXVNNL 240  
 DB 181 LPLDLLNNAITAFSTLEELIRYLEPDRWQVDDSLYKPTWOLLGKAFVGRKSRVVDNL 240  
 QY 241 LKEEYKLYSCTPRNFSVIREELKRTDTTFWPGCLLYKRCGGNCCCLHNCNECCVPRK 300  
 DB 241 LKEEYKLYSCTPRNFSVIREELKRTDTTFWPGCLLYKRCGGNCCCLHNCNECCVPRK 300  
 QY 301 VTRKXHEVLQLRPKTVGKGLHKSLLDVALHHEBECDCVGRNAGG 345  
 DB 301 VTRKXHEVLQLRPKTVGKGLHKSLLDVALHHEBECDCVGRSTGG 345

Search completed: May 27, 2004, 15:44:45  
 Job time : 52 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2004, 15:41:21 ; Search time 36.5 Seconds

(without alignments)  
2982.295 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848  
Sequence: 1 MLVLGLLTLTSALAGQRTGT.....DVLEHHEDCDVCRGNAG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	11	Q9QY71 mus musculus
2	1846	99.9	345	11	Q8C119 mus musculus
3	1819	98.4	345	11	Q9JHV8 Q9JHV8 mus musculus
4	1801	97.5	345	11	Q9E0X6 Q9E0X6 rat mus musculus
5	1667	90.2	345	4	Q9UL22 Q9UL22 homo sapien
6	1664	90.0	345	4	Q9NR41 Q9NR41 homo sapien
7	1552	84.0	345	13	Q91946 Q91946 gallus galli
8	1375	74.4	345	11	Q8K429 Q8K429 rat mus musculus
9	754	40.7	370	4	Q9GZP0 Q9GZP0 homo sapien
10	752	40.6	364	4	Q9BWS5 Q9BWS5 homo sapien
11	750.5	40.4	370	11	Q92517 Q92517 mus musculus
12	746.5	40.4	261	11	Q8K213 Q8K213 mus musculus
13	440.5	23.8	261	11	Q8K213 Q8K213 mus musculus
14	201	10.9	923	13	Q8QFX6 Q8QFX6 brachydanio
15	201	10.9	923	13	Q8AXP1 Q8AXP1 brachydanio
16	192.5	10.4	691	13	Q57658 Q57658 gallus galli

17	192	10.4	34	11	Q9Jm4 mus musculus
18	191	10.3	977	13	Q91925 Q91925 xenopus lae
19	186	10.1	735	13	Q5781 xenopus lae
20	185	10.0	926	4	Q9U00 Q9U00 mus sapien
21	185	10.0	1015	4	Q9Y6L7 Q9Y6L7 mus sapien
22	183	9.9	1012	11	Q9WV6 mus musculus
23	181	9.8	241	11	Q92135 Q92135 rat mus musculus
24	176	9.5	609	4	Q96190 Q96190 homo sapien
25	176	9.5	644	4	Q961H5 Q961H5 homo sapien
26	176	9.5	704	4	Q9H2E1 Q9H2E1 homo sapien
27	176	9.5	923	4	Q86T59 Q86T59 homo sapien
28	175	9.5	1007	13	Q8J128 Q8J128 xenopus lae
29	174.5	9.4	3623	4	Q60492 Q60492 homo sapien
30	169	9.1	1008	13	Q9DER7 Q9DER7 gallus galli
31	168	9.1	921	11	Q9QX38 Q9QX38 rat mus musculus
32	165	8.9	1013	11	Q62381 Q62381 mus musculus
33	165	8.9	1019	13	Q57382 Q57382 xenopus lae
34	162	8.8	1013	4	Q9N0S4 Q9N0S4 mus sapien
35	162	8.8	1013	4	Q43897 Q43897 homo sapien
36	161.5	8.7	905	13	Q800L4 Q800L4 gallus galli
37	161.5	8.7	919	13	Q8UVR0 Q8UVR0 gallus galli
38	161.5	8.7	936	13	Q8UVQ9 Q8UVQ9 gallus galli
39	160	8.7	3623	11	Q70244 Q70244 rat mus musculus
40	158.5	8.6	145	11	Q8BP20 Q8BP20 mus musculus
41	158.5	8.6	413	13	Q7SY25 Q7SY25 brachydanio
42	158.5	8.6	926	11	Q8QZY7 Q8QZY7 mus musculus
43	158	8.5	3620	6	Q9TU53 Q9TU53 canis famli
44	157	8.5	276	4	Q9BRH3 Q9BRH3 homo sapien
45	157	8.5	415	4	Q9UK29 Q9UK29 homo sapien

## ALIGNMENTS

RESULT 1

Q9QY71 PRELIMINARY; PRT; 345 AA.

AC Q9QY71;

DT 01-MAY-2000 (TREMURel. 13, Created)

DT 01-MAY-2000 (TREMURel. 13, Last sequence update)

DT 01-OCT-2003 (TREMURel. 25, Last annotation update)

DE Fallocein (Platelet-derived growth factor C).

GN PDGFC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RA Tsai Y.-U., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;

RT "cDNA cloning of fallocein from mouse ovary."

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.;

RA Gilbertson D., West J., O'Hara P.J.;

RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor."

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;

RA MEDLINE=22354683; PubMed=12466851;

RA THE PANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

RL Nature 420:563-573 (2002).

CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL; AF117608; AAF22516.1; -.

EMBL; AF266467; AAK58566.1; -.



Query Match 98.4%; Score 1819; DB 11; Length 345;  
 Best Local Similarity 98.8%; Pred. No. 2,6e-163;  
 Matches 341; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLLIGLLITSLAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60  
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 DB 61 PKPHTYPRMNVLMWRVAADENVRIQLTPDERGLEDPEDDICKYDFVEVEBSSDQSVL 120  
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 DB 241 LKEEVKLYSCTPRNFVSIRBELKRTDTTFMPGCLLYKRCGNCACCLHNCBQCVPK 300  
 QY 301 VTKKYHEVLOLRPKTVGKGLHKSITDVALBHEBECDCVCRGNAG 345  
 DB 301 VTKKYHEVLOLRPKTVGKGLHKSITDVALBHEBECDCVCRGNAG 345

## RESULT 4

Q9EOX6 PRELIMINARY; PRT; 345 AA.

AC 09EOX6; (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Spinal cord-derived growth factor.  
 GN RSCDGF.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Histar; TISSUE=Kidney;  
 RX MEDLINE=21092670; Pubmed=1162582;  
 RA Hamada T., Ui-Tel K., Imaki Y., Miyata Y.;  
 RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to  
 RT SCDF/PDGF-C/falliclein.";  
 RL Biochem. Biophys. Res. Commun. 280:733-737(2001).  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AB033830; BAB19969.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0008083; F:growth factor activity; IEA.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR000072; PD\_growth\_factor.  
 DR Pfam; Pf00431; CUB; 1.  
 DR Pfam; Pf00341; PDGF; 1.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00141; PDGF; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PSS0278; PDGF; 2; 1.  
 SQ SEQUENCE 345 AA; 38734 MW; F296DA689B765D10 CRC64;

Query Match 97.5%; Score 1801; DB 11; Length 345;  
 Best Local Similarity 96.8%; Pred. No. 1.3e-161;  
 Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLLIGLLITSLAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60  
 DB 1 MLLIGLLITSLAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHRRVVTISGNGSIHS 60

QY 61 PKPHTYPRMNVLMWRVAADENVRIQLTPDERGLEDPEDDICKYDFVEVEBSSDQSVL 120  
 DB 61 PKPHTYPRMNVLMWRVAADENVRIQLTPDERGLEDPEDDICKYDFVEVEBSSDQSVL 120  
 QY 121 GRWGSSTGVGKQTSKGNHRIREFVSDYFSPSEBPGFCIHYSIIMPQVETTSFSLPPSS 180  
 DB 121 GRWGSSTGVGKQTSKGNHRIREFVSDYFSPSEBPGFCIHYSIIMPQVETTSFSLPPSS 180  
 QY 181 LSLDLNNAAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKRVNMLNT 240  
 DB 181 LSLDLNNAAVTAFTLEELIRYLEPDRWQVLDLSLYKPTWQLGKAFLYGKSKRVNMLNT 240  
 QY 241 LKEEVKLYSCTPRNFVSIRBELKRTDTTFMPGCLLYKRCGNCACCLHNCBQCVPK 300  
 DB 241 LKEEVKLYSCTPRNFVSIRBELKRTDTTFMPGCLLYKRCGNCACCLHNCBQCVPK 300  
 QY 301 VTKKYHEVLOLRPKTVGKGLHKSITDVALBHEBECDCVCRGNAG 345  
 DB 301 VTKKYHEVLOLRPKTVGKGLHKSITDVALBHEBECDCVCRGNAG 345

## RESULT 5

Q9UL22 PRELIMINARY; PRT; 345 AA.

AC 09UL22;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).  
 GN HSCDGF OR PDGFC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Tsai Y.J., Lee R.K.K., Lin S.P.;  
 RT "Falloletin, a novel growth factor like gene identified in human  
 RT uterus.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20317014; Pubmed=10858496;  
 RA Hamada T., Ui-Tel K., Miyata Y.;  
 RT "A novel gene derived from developing spinal cords, SCDF, is a unique  
 RT member of the PDGF/VBGF family.";  
 RL FEBS Lett. 475:97-102(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21347863; Pubmed=11297552;  
 RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,  
 RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,  
 RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.B.;  
 RT "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That  
 RT Binds to PDGF alpha and beta Receptor.";  
 RL J. Biol. Chem. 276:27406-27414(2001).  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AF091434; AAF00049.1; -;  
 DR EMBL; AB033831; BAB03266.1; -;  
 DR EMBL; AF260738; AAK51637.1; -;  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0008083; F:growth factor activity; TAS.  
 DR GO; GO:0007417; P:central nervous system development; TAS.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR000072; PD\_growth\_factor.  
 DR Pfam; Pf00431; CUB; 1.  
 DR Pfam; Pf00341; PDGF; 1.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF 2; 1.  
SQ SEQUENCE 345 AA; 39029 MW; CDB9E51F40633E78 CRC64;

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6e-149;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

```

QY 1 MLLGLLLTSLAGRTGTRAEISNLSKQLQSDKQGVDPDRHRYVTISGNSIHS 60
DB 1 MSIFGLLLTSLAGRGRTQAEISNLSKQFQSSNKEQGVDPDRHRYVTISGNSIHS 60
QY 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPSDGYL 120
DB 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPSDGYL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGCIHYSTIMPOVTTSPVLPSS 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGCIHYSTIMPOVTTSPVLPSS 180
QY 181 LSLDLLNNAVTAFTSTEEILRYLEPPRWQVDDLSLYKPTWQLGKAFLYGKSKVYNL 240
DB 181 LSLDLLNNAVTAFTSTEEILRYLEPPRWQVDDLSLYKPTWQLGKAFLYGKSKVYNL 240
QY 241 LKEEVLVYSCPTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVLVYSCPTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKHHEVQLRPKTVGKGLHSLTDVLALEHHEBCDCVCRGNAGG 345
DB 301 VTKKHHEVQLRPKTVGKGLHSLTDVLALEHHEBCDCVCRGNAGG 345

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## RESULT 6

Q9NR1 PRELIMINARY; PRT; 345 AA.  
ID Q9NR1;  
AC Q9NR1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Platelet-derived growth factor C.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=lung;  
RX MEDLINE=20268201; PubMed=10806482;  
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uteila M.,  
RA Backstrom G., Hellstrom M., Boström H., Li H., Soriano P.,  
RA Bertholz C., Heidt C.-H., Alltalo K., Ostman A., Eriksson U.;  
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-  
receptor."  
RL Nat. Cell Biol. 2:302-309 (2000).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
CC EMBL; AF244813; AAF80597.1; -;  
DR Genew; HGNC:8801; PDGFC.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008083; F:growth factor activity; IEA.  
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF 2; 1.  
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CCEA CRC64;

Query Match 90.0%; Score 1664; DB 4; Length 345;  
Best Local Similarity 86.7%; Pred. No. 1.2e-148;

Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

```

QY 1 MLLGLLLTSLAGRTGTRAEISNLSKQLQSDKQGVDPDRHRYVTISGNSIHS 60
DB 1 MSIFGLLLTSLAGRGRTQAEISNLSKQFQSSNKEQGVDPDRHRYVTISGNSIHS 60
QY 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPSDGYL 120
DB 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPSDGYL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGCIHYSTIMPOVTTSPVLPSS 180
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGCIHYSTIMPOVTTSPVLPSS 180
QY 181 LSLDLLNNAVTAFTSTEEILRYLEPPRWQVDDLSLYKPTWQLGKAFLYGKSKVYNL 240
DB 181 LSLDLLNNAVTAFTSTEEILRYLEPPRWQVDDLSLYKPTWQLGKAFLYGKSKVYNL 240
QY 241 LKEEVLVYSCPTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVLVYSCPTPRNFSVSIREEIKRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKHHEVQLRPKTVGKGLHSLTDVLALEHHEBCDCVCRGNAGG 345
DB 301 VTKKHHEVQLRPKTVGKGLHSLTDVLALEHHEBCDCVCRGNAGG 345

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## RESULT 7

Q91946 PRELIMINARY; PRT; 345 AA.  
ID Q91946;  
AC Q91946;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Spinal cord-derived growth factor.  
GN SCDGF.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=white Leghorn; TISSUE=Spinal cord;  
RX MEDLINE=20317014; PubMed=10858496;  
RA Hamada T., Ui-Tei K., Miyata Y.;  
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique  
member of the PDGF/VEGF family."  
RL FEBS Lett. 475:97-102 (2000).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
CC EMBL; AB033829; BAB03265.1; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008083; F:growth factor activity; IEA.  
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.  
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF 2; 1.  
SQ SEQUENCE 345 AA; 38940 MW; 97ACBA992BF5128C CRC64;

Query Match 84.0%; Score 1552; DB 13; Length 345;  
Best Local Similarity 80.3%; Pred. No. 4.5e-138;  
Matches 277; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

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QY 1 MLLGLLLTSLAGRTGTRAEISNLSKQLQSDKQGVDPDRHRYVTISGNSIHS 60
DB 1 MSIFGLLLTSLAGRGRTQAEISNLSKQFQSSNKEQGVDPDRHRYVTISGNSIHS 60
QY 61 PKFPHTPRNMYLVRLVAVDENVRVQLTFDERFGLEDEDDICKYDFVEVEPSDGYL 120

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Db 61 PKPHTYPRNTVLVWRLVAVDENVMIQLTFDERFGLDEPDDICXDPEVEEPESDGTVL 120
Qy 121 GRMGSGTVPGKQSKGNHIRIRFVSDPEFSEPGFCHYSIIMPQVETTSPTVLPSS 180
Db 121 GRMGSSSSVPSRQISKGNQIRIRFVSDPEFSPQPCFCHYLLVPHHTEAPSSLPSPA 180
Qy 181 LSLDLNNAVAFSTLEBELIRYLEPDRQVLDLSLYKPTWQLGKAFLYGKSKYVNL 240
Db 181 LPLDVNNANAVGFSTVEBELIRYLEPDRQVLDLSLYKPTWQLGKAFYHGRKSRVLDNL 240
Qy 241 LKEEVLYSCTPRNFSVSIRESLKRDTTIFMPCGLLVRCGACACCLHNCQCVRK 300
Db 241 LKEEVRLYSCTPRNFSVSLREELKRTDTIFMPLCLLVRCGACACCHQNCQCVRPTK 300
Qy 301 VTKKYHEVLQRPKTVKGLKSLTDVALHEHESDCVCRNAG 345
Db 301 VTKKYHEVLQRPKTVKGLKSLTDVPLEHESDCVCRKNSBG 345

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## RESULT 8

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ID 08K429 PRELIMINARY; PRT; 258 AA.
AC 08K429;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
Healing."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF508348; AAM47265.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 258
SQ SEQUENCE 258 AA; 29255 MW; 88625B989FCC3F8B CRC64;

Query Match 74.4%; Score 1375; DB 11; Length 258;
Best Local Similarity 96.9%; Pred. No. 1.6e-121;
Matches 250; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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Qy 282 GNCACCLHNCQCVR 299
Db 241 GNCACCLHNCQCVR 258

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## RESULT 9

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ID 09GZP1 PRELIMINARY; PRT; 370 AA.
AC 09GZP1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN RSCDGF-B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ue-Tai K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
SCDF/PDGF-C/fallicoin."
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB052170; BAB18920.1; -.
DR PIR; JC7592; JC7592.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;

Query Match 40.8%; Score 754; DB 11; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.3e-62;
Matches 151; Conservative 62; Mismatches 86; Indels 28; Gaps 10;

```

## RESULT 10

```

ID 09GZP0 PRELIMINARY; PRT; 370 AA.

```

AC Q9GZP0. 01-MAR-2001 (TREMBLrel. 16. Created)  
AD DT 01-MAR-2001 (TREMBLrel. 16. Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)  
DE SPINAL\_CORD-derived growth factor-B (MSGP36) (IRIS-expressed growth factor long form) (platelet-derived growth factor D).  
GN HSCGCF-B OR IEGF OR PDGFD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homnidae.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;  
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to SCDF/PDGF-C/fallotein.";  
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Artera;  
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.M., Liu S., Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J., Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q., Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Iris;  
RA Wistow G.;  
RT "Iris-expressed Growth Factor (IEGF).";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX PubMed=11331881;  
RA Bergsten E., Uccella M., Li X., Pietras K., Ostman A., Heldin C.H., Allitalo K., Eriksson U.;  
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-receptor.";  
RL Nat. Cell Biol. 3:512-516(2001).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21231380; PubMed=11331882;  
RA Lachocnelle W.J., Jeffers M., McDonald W.F., Chillaikuru R.A., Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C., Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J., Shinkets R.A., Rothberg J.M., Lichenstein H.S.;  
RT "PDGF D, A Novel Protease-Activated Growth Factor.";  
RL Nat. Cell Biol. 3:517-521(2001).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AB033832; BAB18903.1; -;  
DR EMBL; AF113216; AAG39287.1; -;  
DR EMBL; AY027517; AAK20081.1; -;  
DR EMBL; AF36376; AAK56136.1; -;  
DR EMBL; AF35584; AAK38840.1; -;  
DR PIR; JCT7591; JCT7591.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008083; F:receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0005215; P:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR InterPro; IPR000531; TonB\_boxC.  
DR Pfam; PF00431; CUB; 1.  
DR SMART; SMO0042; CUB; 1.  
DR SMART; SMO0141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS50278; PDGF; 2; 1.  
DR PROSITE; PS00430; TONB\_DEPENDENT\_REC\_1; 1.  
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7B7674 CRC64;

	Matches	148;	Conservative	59;	Mismatches	92;	Indels	28;	Gaps	9
QY	37	FONGVOD--PRHERVVTISGNGSIHSPEKPHYPRNNVLWMLVAVDENVRIOQLTFDERFG	95							
Db	42	ESNNHTLDYRDEFTIQVKGNGVQSPREPPNSYPRNLLTTLRWLHS--QENTRIQLVFDNQFG	100							
QY	96	LEDEPDLDCKYDFYVEEPEPDSGVLV--GRMGSGSIVPEPKQSKGNHITIRVSDYEFSE	153							
Db	101	LEAEENDICRVDPEVEDISESTTIRGRMGHKEVPRIRSKRTQIKITERSDYFPAK	160							
QY	154	PGFCIHYSII---MPQVTEFT-----SPSVLPSPSLSLDLNNNAVTAARST	195							
Db	161	PGFKIYISLLEDFQPAASSTNWSYVSSISGVSYNPSSTVDP--TLIDALDLDKIAEFDI	219							
QY	196	LEELIRLYDEPPRWQVODLSDLYKPTWQLGKAFLYGKSKSVNNLNLKEEVLVYSGSTPRNF	255							
Db	220	VEDLLKYNPESWQEDLENNMTLDFPRYGRGRY--HDKRSK--VDLDRINDADARYSGTSPRNY	277							
QY	256	SVSIRIEELKRTDTTFWPEGCLVKRGGNGACCLHNCEQCQVPRKVTYKTYHEVLQLRP--	313							
Db	278	SVNIRIEELKLVNVVFFPRCLLVORCGNGCGGTVMNRSTCNSGKYTKYHEVLQFEBGH	337							
QY	314	-KTGVKGLHSLTDVALLEHHEECQVC	339							
Db	338	IKRGRAKTMALVDIQLDHHERCCTIC	364							

09BWV5	RESULT 11			
ID	09BWV5	PRELIMINARY;	PRT;	364 AA.
AC	09BWV5;			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Iris-expressed growth factor short form (Spinal cord-derived growth factor-B).			
DE	IEGF.			
GN	IEGF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TextID=9606;			
RP	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Iris;			
RA	Wistow G.;			
RT	"Iris-expressed Growth Factor (IEGF)";			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
RP	(2)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RA	Strausberg R.;			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY027518; AAK20082.1; -			
DR	EMBL; BC030645; AAH30645.1; -			
DR	PIR; JC7591; JC7591.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0008083; F:growth factor activity; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0005215; F:transporter activity; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR000859; CUB.			
DR	InterPro; IPR000072; PD.growth_factor.			
DR	InterPro; IPR000531; TonB_boxc.			
DR	Pfam; PF00431; CUB.1.			
DR	PROSITE; PS01180; CUB; 1.			
DR	PROSITE; PS50278; PDGF_2; 1.			
DR	PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.			
SQ	SEQUENCE 364 AA; 42166 MW; 245CS3B8DEA9EAC CRC64;			
Query Match	40.6%;	Score 750.5;	DB 4;	Length 364;
Best Local Similarity	45.6%;	Pred. No. 2.7e-62;		
Matches 145;	Conservative 58;	Mismatches 88;	Indels 27;	Gaps 8;



Qy	45	HERVVT1SGN5SHSPKPTHTYPRMVLVADEVNR1QLTFDEPFGDEPDDIC	104
Db	45	RDEET1QVKGNCYVSPFRPN5YPRNLTLTRH5-QENTRIQ1QVLDNQGLEAENDIC	103
Qy	105	KYDFVEVEBPDSGVLY--GRMGSGVVPCKQTSKGNHIRIRFVSD5EYFSEPFCTIHSV1	162
Db	104	KYDFVEVBDISST5T1IRRMWCGHKEVPRIR5RTMQIITTFPSDDYFAKBP5FK1Y5GL	163
Qy	163	I---MPQVETT-----SPSVLEPSSLSLDLNNAVTA5FT5EELIRYLE	204
Db	164	LEDFOPAAS5ETN5SVTS5SIGSV5N5PSVTD5P-7L1DALDJKIA5EPTV5EDLLKTF5N	222
Qy	205	PDRMGVUD5L5YK5P5WQQLGKAF5YVCK5K5KV5NN1LK5E5V5LY5CT5P5N5FS5T5EELK	264
Db	223	P5WQ5ED5ENMYL5DTP5R5K5GR5Y-HDR5K5K-V5LD5RL5ND5AK5RY5CT5P5N5Y5N5I5REELK	280
Qy	265	RDT5TF5P5G5C5LL5YK5K5G5NC5AC5C5L5H5NC5C5Q5C5V5P5R5V5TK5K5H5E5V5L5D5LP---	321
Db	261	LANV5FP5R5C5LL5VQ5K5G5NC5G5C5GY5N5R5B5CT5C5N5G5TK5Y5K5H5E5V5L5D5P5E5G5I5R5G5R5AKT	340
Qy	322	KS5L5D5VA5LEH5HE5C5D5C5V5C	339
Db	341	MALV5DIQ5LDH5HER5CD5IC	358
RESULT 12			
ID	Q92517	PRELIMINARY;	PRT; 370 AA.
AC	Q92517	OSD118;	
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Platelet-derived growth factor D (18-day embryo whole body cDNA, RIKEN		
DE	full-length enriched library, clone:1110003109		
DE	Product:platelet-derived growth factor D).		
GN	PDGFR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BA1B/c;		
RC	MEDLINE=21231380; PubMed=11331882;		
RA	Labochaille L.J., Jeffers M., McDonald W.F., Chilikuru R.A.,		
RA	Gijsse N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernat C.,		
RA	Bugues C.E., Fernandez E., Degler L.L., Rittman B., Shinkets J.,		
RA	Shinkets R.A., Rochberg J.W., Lichensteih H.S.;		
RT	"PDGF D, A Novel Protease-Activated Growth Factor.";		
RL	Nat. Cell Biol. 3:517-521(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Body;		
RA	Adechi J., Aizawa K., Akahira S., Akiura T., Arai A., Aono H.,		
RA	Arakawa T., Bono H., Caminetti P., Fukuda S., Fukunishi Y., Furuno M.,		
RA	Hasegawa T., Hara A., Hayatsu N., Hizumoto K., Hizooka T., Hori F.,		
RA	Imocanti K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,		
RA	Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,		
RA	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,		
RA	Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K.,		
RA	Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,		
RA	Sojima Y., Suzuki H., Tagami M., Tagawa A., Takahashi K., Tanaka T.,		
RA	Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,		
RA	Muramatsu M., Hayashizaki Y.;		
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Body;		
RC	MEDLINE=22354683; PubMed=12466851;		
RA	THE FANTOM Consortium,		
RA	THE RIKEN Genome Exploration Research Group Phase I & II Team,		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs";		

DB	Query Match	40.4% Best Local Similarity	Score 746.5; 43.5% Matches 151;	DB 11; Pred. No. 6.6e-62; Conservative 63;	Length 370; Mismatches 102; Indels 31;	Gaps 9
RL	Nature 420:563-573 (2002).					
RP	SEQUENCE FROM N.A.					
RN	STRAIN=C57BL/6J; TISSUE=Body;					
RC	MEDLINE=21085660; PubMed=11217851;					
RA	Riken Pantom Consortium;					
RT	"Functional annotation of a full-length mouse cDNA collection.";					
RL	Nature 409:685-690 (2001).					
RN	(5)					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=C57BL/6J; TISSUE=Body;					
RX	MEDLINE=99279253; PubMed=10349636;					
RA	Carninci P., Hayashizaki Y.;					
RT	"High-efficiency full-length cDNA cloning.";					
RL	Meth. Enzymol. 303:19-44 (1999).					
RN	(6)					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=C57BL/6J; TISSUE=Body;					
RX	MEDLINE=20499374; PubMed=11042159;					
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,					
RT	Komoto H., Okazaki Y., Muramatsu M., Hayashizaki Y.;					
RL	"Normalization and subtraction of cap-trapper-selected cDNAs to					
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";					
RL	Genome Res. 10:1617-1630 (2000).					
RN	(7)					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=C57BL/6J; TISSUE=Body;					
RA	MEDLINE=20530913; PubMed=11076861;					
RA	Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,					
RA	Komoto H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,					
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,					
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,					
RA	Fujisawa S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe M.,					
RA	Yoneda Y., Ishikawa T., Ogawa K., Tanaka T., Matsura S., Kawai J.,					
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;					
RT	"Riken integrated sequence analysis (RISA) system-384-format					
RT	sequencing pipeline with 384 multicapillary sequencer.";					
RL	Genome Res. 10:1757-1771 (2000).					
CC	-1 SIMILARITY: CONTAINS 1 CUB DOMAIN.					
DR	EMBL; AF355583; AAK38839.1; -					
DR	EMBL; AK003358; BAB2735.2; -					
DR	MGI; MGI:1919035; Pdgfd.					
DR	GO; GO:0016020; C:membrane; IEA.					
DR	GO; GO:0008083; F:growth factor activity; IEA.					
DR	GO; GO:0008151; P:cell growth and/or maintenance; IEA.					
DR	InterPro; IPR000859; CUB.					
DR	InterPro; IPR000072; PD_growth_factor.					
DR	Pfam; PF00431; CUB; 1.					
DR	SMART; SM00042; CUB; 1.					
DR	SMART; SM00141; PDGF; 1.					
DR	PROSITE; PS01180; CUB; 1.					
DR	PROSITE; PS02078; PDGF 2; 1.					
DR	SEQUENCE 370 AA; 42809 MW; 9808B4CF6813BFBE CXC64;					
QY	Query Match	40.4% Best Local Similarity	Score 746.5; 43.5% Matches 151;	DB 11; Pred. No. 6.6e-62; Conservative 63;	Length 370; Mismatches 102; Indels 31;	Gaps 9
QY	16 QRTGTRASNSISKQLQSSDKEQNGVQDPRRERVYTTISGNSIHSPKPHPTPRMVLVW 75					
DB	26 QRASTKALRNAN---LRRDSNHLTDLYOEENIQVTSNCHVOSPRPNLLTLTW 81					
QY	76 RLVAIVDEIVRQLQFDFRFGLEDEDDICKDFVEVEEPPSGS--VLGRMGCSGVPPGKQ 133					
DB	82 WLRS-QEKTIRQLQSFSDHOFGLAEABNDICRIVFVEEVSSTVYVGRMGCHKEIPRI 140					
QY	134 TSKGNHRIIRFVSDPEYSPBFCIHYSII--MPQVTEY-----SPSV 175					
DB	141 TSTRNQIKITFKSDYFAVAKGFKITYSFVEDPQDEAASERTNWSVTSSFGSVSYHSPSI 200					
QY	176 LPPSSLSLDDLNNAVTAFTSEELIRYLEPPRWQVDDLSLYKPTWQLGKAFLYGKSKV 235					
DB	201 TDP-TLTADADAKTVAEEDYEDLLKHNPNVSWDDDENLVLIDRPHVGRGVR-HDRKSK- 257					



RT "The cloning and expression of neuropilin-1."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB088776; BACS3657.1; -  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0007155; P:cell adhesion; IEA.  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR000421; FA58 C.  
DR InterPro: IPR008979; Gal Bind like.  
DR InterPro: IPR000998; MAM\_domain.  
DR Pfam: PF00431; CUB; 2.  
DR Pfam: PF00754; F5\_f8\_type\_C; 2.  
DR Pfam: PF00629; MAM; 1.  
DR SMART: SM0042; CUB; 2.  
DR SMART: SM00231; FA58C; 2.  
DR SMART: SM00137; MAM; 1.  
DR PROSITE: PS01180; CUB; 2.  
DR PROSITE: PS01285; FA58C\_1; 1.  
DR PROSITE: PS01286; FA58C\_2; 2.  
DR PROSITE: PS50022; FA58C\_3; 2.  
DR PROSITE: PS00740; MAM\_1; 1.  
DR PROSITE: PS50060; MAM\_2; 1.  
SQ SEQUENCE 923 AA; 102541 MW; 0B6CE33ED28A21F7 CRC64;

Query Match 10.9%; Score 201; DB 13; Length 923;  
Best Local Similarity 27.9%; Pred. No. 8.3e-10;  
Matches 63; Conservative 31; Mismatches 74; Indels 58; Gaps 10;

QY 1 MLLIGLLILTSALAGQRTGTAESNLSSKQLQSSDPKEQNGVQDPHREYVTISGNGSIHS 60  
DB 8 ILFTGIPLIVSALNRDKCGDN-----IRITSANYLYTS 39  
QY 61 PKPHTYPRNNVLVWRLVAVDENVRIQLTDERFGLEDPEDDICKYDFVEYEBPSD--GS 118  
DB 40 FGRVSVYPSQKCIWITAPGNORILINFNPHFDLEDRE--CKNDYVEVRDGVDENGQ 96  
QY 119 VLGRWCGSGTVPGKQTSKGNHRIKRVSDYFSPSEPGFCIHYSIIM--PQYTE--TISPS 174  
DB 97 LVGKYCGK-IAPSPVSSGNQLFIKFVSD-YETHGAGFSIRYEIFKGTPECSRNTSSSG 154  
QY 175 VLP-----PSSLSLDL-----LNNAVTAFSTLEELIRYLEPD 206  
DB 155 VIKSPGPEPEKYPNNDCTFMIFAPMSRIVLEFESFE-----LEPD 195

Search completed: May 27, 2004, 15:46:43  
Job time : 37.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2004, 15:41:56 ; Search time 14 Seconds  
(without alignments)  
2370.434 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLGLLLSALAGQRTGT.....DVALEHHECDVCGRNAGG 345

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	754	40.8	370	2 JC7592	spinal cord-derivative
2	753	40.7	370	2 JC7591	spinal cord-derivative
3	746.5	40.4	370	2 JC7598	platelet-derived g
4	191	10.3	707	2 JC2218	procollagen C-endo
5	190	10.3	823	1 A58788	procollagen C-endo
6	183.5	9.9	730	1 BMHU	procollagen C-endo
7	183.5	9.9	927	1 J00948	AS antigen precursor
8	181	9.8	986	1 B58788	procollagen C-endo
9	181	9.8	986	1 B58788	procollagen C-endo
10	174.5	9.4	3623	2 T09456	intrinsic factor-B
11	160	8.7	3623	2 T08618	intrinsic factor-B
12	158	8.5	449	2 A55362	procollagen I C-pr
13	153	8.3	1057	1 A59288	procollagen I C-pr
14	147.5	8.0	1524	2 T30337	polypeptide - Afri
15	145.5	7.9	686	1 A59271	Ra-reactive factor
16	144	7.8	699	1 I54763	Ra-reactive factor
17	143.5	7.8	597	2 S71352	metalloproteinase
18	141.5	7.7	1070	2 T31069	collagen-BMP-1 like
19	140.5	7.6	3871	2 T22812	hypothetical prote
20	139	7.5	1594	2 T30549	hemisin - rabbit
21	137.5	7.4	705	1 C1HURB	development subcomp
22	135.5	7.3	1464	2 S58984	development protei
23	133.5	7.2	402	2 JH0403	procollagen I C-pr
24	128	6.9	277	2 A41735	hyaluronate-bindin
25	127	6.9	419	2 S69207	vascular endotheli
26	126.5	6.8	579	2 JC7629	membrane-type Iiz
27	125.5	6.8	245	1 T30018	platelet-derived g
28	125.5	6.8	767	2 T30018	hypothetical prote
29	125	6.8	533	2 JC7985	brain-specific CUB

30	123	6.7	275	2 JC6506	tumor necrosis fac
31	122.5	6.6	2403	2 A59386	sanko - human
32	119.5	6.5	2083	2 T42721	CRP-ductin-alpha p
33	117.5	6.4	276	2 A47280	TSG-6 homolog PS4
34	117.5	6.4	1290	2 A57190	ebnerin precursor
35	114.5	6.2	200	2 I51551	platelet-derived g
36	114.5	6.2	215	2 S08220	platelet-derived g
37	114.5	6.2	226	2 I51550	platelet-derived g
38	113	6.1	695	1 S05008	complement subcomp
39	112.5	6.1	241	1 PFH052	complement subcomp
40	111.5	6.0	226	1 FWH052	platelet-derived g
41	109	5.9	694	2 JC6554	PDGF-related trans
42	108.5	5.9	148	2 D49530	complement subcomp
43	107	5.8	321	2 T33161	16K vascular endot
44	104	5.6	319	2 I51569	hypothetical prote
45	103.5	5.6	225	2 S25097	UVS.2 protein - Af
					platelet-derived g

## ALIGNMENTS

## RESULT 1

spinal cord-derived growth factor-B precursor - rat  
C:Species: Rattus norvegicus (Norway, rat)  
C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001  
C:Accession: JC7592  
R:Hamada, T.; Oi-Tel, K.; Imaki, J.; Miyata, Y.  
Biochem. Biophys. Res. Commun. 280, 733-737, 2001  
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C  
A:Reference number: JC7591; MUID:21092670; PMID:11162582  
A:Contents: Fetal brain  
A:Accession: JC7592  
A:Molecule type: mRNA  
A:Residues: 1-370 <HAM>  
A:Cross-references: DDBJ:AB052170  
C:Genetics:  
A:Gene: scdGF-B  
F:1-17/Domain: secretory signal sequence #status predicted <SIG>  
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>  
F:52-170/Region: CUB domain #status predicted  
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gro  
F:294-308/Region: conserved motif #status predicted

Query Match	Score	Match	Length	DB 2;	Length	370;
Best Local Similarity	46.24;	Pred. No.	1.4e-55;			
Matches 151;	Conservative 62;	Mismatches 86;	Indels 28;	Gaps 10;		
37	EONGVOD-PHERVITISGSGSIHSPKPTPRNVLVRLVAVDENVRIQLTFDRFG	95				
42	ESNHLTLVLRDENIRVTGTGHVQSPFPNSYPNNLLTWRLHS-QEKTRIQLAFFDQFG	100				
96	LEDEDDICIKYFEVEVERPSDGS--VLGRMGSGTGVGKOTSGKNHRIKRVFSDEYPSSE	153				
101	LEBAENDICRYDFEVEDVSESSITVGRKCGKHEIPRTSRNOKIKIFQSDIYVAK	160				
154	PGFCIHYSIT--MPQ-----VTET-----TSPSYLPPSSSLDLNNAVTAFT	195				
161	PGFKIYVSFVEDQPEAASEINNESVTSFSGVSYHPSVM-DSTLADALDKAIAFDFT	219				
196	LEELIRYLEPDRQVODLSLYKPTWOLGKAFYLGKSKYVNLNLEKRYKVSCTPRNF	255				
220	VEDLLKTFNPASWODDLENLYMTPRYGRSY-HERSK-VLDRLNDVRYSCTRNH	277				
256	SVSIRBELKRTDTIFMPGCLLVKRCGNCACCLHNCQCVPRKVTYKKEHVLQLRP--	313				
278	SVNIREELKLTNAVFFPRCLLVORCGNCCCGTLNWKSCITSSGKVTYKKEHVLKPRGH	337				
314	KTGVKGLKSLTDVVALEHHECDVCVC	339				
338	FKRGRKAKNALVDIQLDHHERCDIC	364				



N:Alternate names: bone morphogenic protein splice form BMP-1/His  
C:Species: Homo sapiens (man)  
C:Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 18-Jun-1999  
A:Accession: A37278; A58788  
R:Mooney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, L.M.; Whitters, M.J.; Kriz, R.W.; Hew  
Science 242, 1528-1534, 1998  
A:Title: Novel regulators of bone formation: molecular clones and activities.  
A:Reference number: A37278; MUID:89072730; PMID:3201241  
A:Accession: A37278  
A:Molecule type: mRNA  
A:Residues: 1-702, 'EKRPALOPRGRHOLKFRVQKRRTPQ' <WO2>  
A:Cross-references: GB:M22488; NID:g179499; PIDN:AA51833.1; PID:g179500  
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.  
J. Biol. Chem. 269, 35572-35278, 1994  
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (tmld) are encoded  
A:Reference number: A58788; MUID:95096114; PMID:7798260  
A:Accession: A58788  
A:Molecule type: mRNA  
A:Residues: 703-823 <TRK>  
A:Cross-references: GB:LJ5278; NID:g619423; PIDN:MAC41703.1; PID:g619424  
A:Gene: GDB:BMP1; BMP-1  
A:Cross-references: GDB:125203; OMIM:112264  
A:Map position: 8p21-8p21  
C:Function:  
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type  
A:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E  
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g  
F:1-32/Domains: signal sequence #status predicted <SIG>  
F:23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>  
F:130-331/Domains: astacin homology <AST>  
F:322-431/Domains: C1r/C1s repeat homology <C1R1>  
F:435-544/Domains: C1r/C1s repeat homology <C1R2>  
F:551-587/Domains: EGF homology <EGF>  
F:591-700/Domains: C1r/C1s repeat homology <C1R3>  
F:738-752/Region: histidine-rich  
F:911,142,333,363,559/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:163-319,185-205,323-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-666  
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted  
F:214/Active site: Glu #status predicted  
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match	10.3%	Score 190;	DB 1;	Length 823;
Beat Local Similarity	36.0%	Pred. No. 9.9e-08;		
Matches 54;	Conservative 20;	Mismatches 48;	Indels 28;	Gaps 7;
QY	55	NGSISKRPHTPTNNMLVRLVAVDENVRIGLTFDRFGLEDPEEDICKDYFVEE	113	
DB	599	NGSISPMQPKPEYPPNKNCIQVLVPTQ--YRISLFD--PFEEGNDVCKYDFEVRSG	654	
QY	114	-PSDSVLGRMGCGSTVGKOTSGKNHRIKRPVSDPEFPSEPGCIY-----	160	
DB	655	LTADSKLGGKCGS-EKREVITISQYNNKRVFKSDNTV-SKKGFAPFPVLEGAQRHS	712	
QY	161	-----SIIMQVTEETSPSVLPSSLSLD	184	
DB	713	HLSGELLLCPHALVDVTVA--PPEALHGD	740	

RESULT 6  
BHMU1  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human  
N:Alternate names: bone morphogenic protein 1 (BMP1)  
C:Species: Homo sapiens (man)  
C:Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999  
A:Accession: A37278; B58788  
R:Mooney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, L.M.; Whitters, M.J.; Kriz, R.W.; Hew  
Science 242, 1528-1534, 1998  
A:Title: Novel regulators of bone formation: molecular clones and activities.  
A:Reference number: A37278; MUID:89072730; PMID:3201241  
A:Accession: A37278  
A:Molecule type: mRNA  
A:Residues: 1-730 <WO2>

A.Cross-references: GB:M22468; MID:g179499; PIDN:AAS1833.1; PID:g179500  
A.Gene: GDB:BMP1  
A.Cross-references: GDB:I25203; OMIM:112264  
A.Map position: 8p21-8p21  
C.Function:  
I.Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type I.  
C.Superfamily: procollagen C-endopeptidase; aspartic homology; Clr/Cls repeat homology;  
C.Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g  
F.1-22/Domain: signal sequence #status predicted <Sig>  
F.123-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <Mat>  
F.1130-1321/Domain: aspartin homology <AsP>  
F.1322-431/Domain: Clr/Cls repeat homology <Clr1>  
F.1435-544/Domain: Clr/Cls repeat homology <Clr2>  
F.1551-587/Domain: EGF homology <EGF>  
F.1591-700/Domain: Clr/Cls repeat homology <Clr3>  
F.191\_142-333,363,569/Binding site: carbonyl-terminus (covalent) #status predicted  
F.163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-6  
F.1213\_217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted  
F.1214/Active site: Glu #status predicted  
F.1565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match            9.% Score 183.5; DB 1; Length 730;  
Beet Local Similarity 38.9%. Pred. No. 3e-07;  
Matches 49; Conservative 18; Mismatches 44; Indels 15; Gaps 6;

OY       NGSIHSPFPPTTYPRNMVLVAVDENVRILQTFEDRFGLEDEDDICKYFEVER- 113  
        ||||| :||::||::||:||||| :||:|||||  
Db       599 NGSIHSPMPPEPPKNCIKQLVAPlQ-VRIISLQFD--PFETGNDVCCKDFEVRSG 654

OY       114 -PSDGSVLGRMGSGTGVFKOTSKGNHRIRNFVSDEYRPSEBGCIFHSIIIMPQTETS 172  
        :::::::||::||::||:||||| :||:|||||  
Db       655 LTADSKHLKGRFCGS-EKEPVITTSQYNMKRVFFKSNDTV-SKKGFRAHF-----FSKR 705

OY       173 PSVLAP 178  
        ||::||  
Db       706 PALOP 711

RESULT 7  
J00948  
AS antigen precursor - African clawed frog  
C.Species: Xenopus laevis (African clawed frog)  
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C.Accession: J00466; J00948  
R.Takagi S.; Hirata T.; Agata K.; Mochizuki M.; Eguchi G.; Fujisawa H.  
Neuron 7, 295-307, 1991  
A.Title: The AS antigen, a candidate for the neuronal recognition molecule, has homologues  
A.Reference number: J00466; PMID:91337458; PMID:1908252  
A.Accession: J00466  
A.Molecule type: mRNA  
A.Residues: 1-927 <Tak>  
A.Cross-references: GB:D10467; GB:D01077; MID:g222962; PIDN:BAO1260.1; PID:g222963  
A.Experimental source: tadpole, brain  
A.Note: This protein has motifs homologous to complement components C1r and C1s and to C2. Comment: This protein is a neuronal cell surface molecule involved in the neuronal recognition family: Xenopus AS antigen; Clr/Cls repeat homology; discoidin I amino-terminal C-keyword: duplication; glycoprotein; transmembrane protein  
F.1-21/Domain: signal sequence #status predicted <Sig>  
F.122-927/Product: AS antigen #status predicted <ASA>  
F.127-138/Domain: Clr/Cls repeat homology <CLR1>  
F.147-262/Domain: Clr/Cls repeat homology <CLR2>  
F.274-424/Domain: discoidin I amino-terminal homology <DN1>  
F.430-584/Domain: discoidin I amino-terminal homology <DN2>  
F.1646-812/Domain: MAM homology <MAM>  
F.1861-883/Domain: transmembrane #status predicted <TM>  
F.150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match            9.% Score 183.5; DB 1; Length 927;  
Beet Local Similarity 30.7%. Pred. No. 4.1e-07;  
Matches 55; Conservative 34; Mismatches 65; Indels 25; Gaps 9;

50 VTIGNGSHSPFPPTTYPRNMVLVAVDENVRILQTFEDRFGLEDEDDICKYDFV 109

```

      31 IKITSPSYLTSAQYPHSPSPORCEWILQAPHEYORIMINPHFDLEDE---CKYDYV 87
      110 EV--EESPDSYVGRMCGSTGVGKQTSKGNHIRIRFVSDEYFSPGFCIHYSIIM--P 165
      88 EVIDGDANAOQLGKTCGK-IADSPVLTSPSIFIRFVSDEYFPG-AGSFIRYEVFKTP 145
      166 QVTE--TTSPSVLP-----PSSLSDLLNNVAFASTLEELIRYLEPDRWQVLDLS 214
      146 ECSRNFSTSNGVKSPKPYEKYFNALACTYIIFA---PMQGITV--LRESEPLEADS 198

      Db
      31 IKITSPSYLTSAQYPHSPSPORCEWILQAPHEYORIMINPHFDLEDE---CKYDYV 87
      110 EV--EESPDSYVGRMCGSTGVGKQTSKGNHIRIRFVSDEYFSPGFCIHYSIIM--P 165
      88 EVIDGDANAOQLGKTCGK-IADSPVLTSPSIFIRFVSDEYFPG-AGSFIRYEVFKTP 145
      166 QVTE--TTSPSVLP-----PSSLSDLLNNVAFASTLEELIRYLEPDRWQVLDLS 214
      146 ECSRNFSTSNGVKSPKPYEKYFNALACTYIIFA---PMQGITV--LRESEPLEADS 198

      QY
      166 QVTE--TTSPSVLP-----PSSLSDLLNNVAFASTLEELIRYLEPDRWQVLDLS 214
      146 ECSRNFSTSNGVKSPKPYEKYFNALACTYIIFA---PMQGITV--LRESEPLEADS 198

      Db
      146 ECSRNFSTSNGVKSPKPYEKYFNALACTYIIFA---PMQGITV--LRESEPLEADS 198

      RESULT 8
      B58788
      procollagen C-endopeptidase (EC 3.4.24.19) precursor, collagen-like splice form - human
      N:Alternate names: bone morphogenic protein 1, collagen-like splice form
      C:Species: Homo sapiens (man)
      C>Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
      C/Accession: A37278; B58788
      R/Mozney, J.M.; Rosen, V.; Celeste, A.J.; Miltsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
      Science 242, 1528-1534, 1998
      A>Title: Novel regulators of bone formation: molecular clones and activities.
      A:Reference number: A37278; PMID:89072730; PMID:3201241
      A:Accession: A37278
      A:Molecule type: mRNA
      A:Residues: 1-702; 'EKRPALQPPGRPHQLKFRVQKRNTPQ' <WOZ>
      A/Cross-references: GB:M22488; NID:9179499; PIDN:AAA5183.1; PID:9179500
      R/Takahara, K.; Lyons, G.E.; Greenspan, D.S.
      J. Biol. Chem. 269, 32572-32578, 1994
      A>Title: Bone morphogenetic protein-1 and a mammalian collagen-like homologue (mTld) are encoded
      A:Reference number: A58788; PMID:95096114; PMID:7798260
      A:Accession: B58788
      A:Molecule type: mRNA
      A:Residues: 703-986 <TAK>
      A/Cross-references: GB:I35279; NID:9619860; PIDN:AAC41710.1; PID:9619861
      C/Genetics: GDB:BMP1; BMP-1
      A:Gene: GDB:125203; OMIM:112264
      A/Cross-references: GDB:125203; OMIM:112264
      A/Map position: 8p21-8p21
      C/Function:
      A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
      C/Superfamily: procollagen C-endopeptidase; aspartic homology; C1r/C1s repeat homology;
      C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; 91
      F:1-22/Domain: signal sequence #status predicted <SIG>
      F:23-986/Product: procollagen C-endopeptidase collagen-like splice form #status predicted
      F:130-321/Domain: aspartic homology <AST>
      F:322-431/Domain: C1r/C1s repeat homology <C1R1>
      F:435-544/Domain: C1r/C1s repeat homology <C1R2>
      F:551-587/Domain: EGF homology <EG1>
      F:591-700/Domain: C1r/C1s repeat homology <C1R3>
      F:707-742/Domain: EGF homology <EG2>
      F:747-856/Domain: C1r/C1s repeat homology <C1R4>
      F:860-973/Domain: C1r/C1s repeat homology <C1R5>
      F:911-122,332,363,599/Binding site: carboxylate (asn) (covalent) #status predicted
      F:163-119,185-205,332-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
      F:213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted
      F:214/Active site: Glu #status predicted
      F:565,720/Modified site: erythro-beta-hydroxyasparagine (asn) #status predicted

      Query Match
      Best Local Similarity 9.8%; Score 181; DB 1; Length 986;
      Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;

      QY
      55 NSGHSKPPHTPRNNVLMRLVAVDENVRITLTPERGLDEPDIDCKYFVEVE- 113
      599 NSGHSKPPHTPRNNVLMRLVAVDENVRITLTPERGLDEPDIDCKYFVEVE- 654

      Db
      599 NSGHSKPPHTPRNNVLMRLVAVDENVRITLTPERGLDEPDIDCKYFVEVE- 654

      QY
      114 -PSDGSVLGRMCGSTGVPGKQTSKGNHIRIRFVSDEYFSPGFCIHY 160
      655 LTRDSKLGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 700

      Db
      655 LTRDSKLGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 700

      RESULT 9

      149540
      procollagen C-endopeptidase (EC 3.4.24.19) precursor, collagen-like splice form - mouse
      C/Species: Mus musculus (house mouse)
      C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
      C/Accession: I49540
      R/Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
      Dev. Biol. 163, 175-183, 1994
      A>Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is re
      A:Reference number: I49540; PMID:94229342; PMID:8174772
      A:Accession: I49540
      A:Status: preliminary; translated from GB/EMBL/DBJ
      A:Molecule type: mRNA
      A:Residues: 1-991 <RES>
      A/Cross-references: GB:I24755; NID:9439606; PIDN:AAA37306.1; PID:9439607
      C/Genetics:
      A:Gene: Bmp-1
      C/Superfamily: procollagen C-endopeptidase; aspartic homology; C1r/C1s repeat homology;
      C/Keywords: hydrolyase; metalloproteinase; zinc
      F:135-326/Domain: aspartic homology <AST>
      F:356-592/Domain: EGF homology <EG1>
      F:596-705/Domain: C1r/C1s repeat homology <C1R>
      F:712-747/Domain: EGF homology <EG2>
      F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
      F:219/Active site: Glu #status predicted

      Query Match
      Best Local Similarity 9.8%; Score 181; DB 2; Length 991;
      Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;

      QY
      55 NSGHSKPPHTPRNNVLMRLVAVDENVRITLTPERGLDEPDIDCKYFVEVE- 113
      604 NSGHSKPPHTPRNNVLMRLVAVDENVRITLTPERGLDEPDIDCKYFVEVE- 659

      Db
      604 NSGHSKPPHTPRNNVLMRLVAVDENVRITLTPERGLDEPDIDCKYFVEVE- 659

      QY
      114 -PSDGSVLGRMCGSTGVPGKQTSKGNHIRIRFVSDEYFSPGFCIHY 160
      660 LTRDSKLGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705

      Db
      660 LTRDSKLGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705

      RESULT 10
      T09456
      intrinsic factor-B12 receptor Cubilin precursor - human
      C/Species: Homo sapiens (man)
      C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
      C/Accession: T09456
      R/Kozyrak, R.; Kristiansen, M.; Slihaeroglu, A.; Hansen, C.; Tommerup,
      Blood 91, 3593-3600, 1998
      A>Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteri-
      A:Reference number: Z16677; PMID:98241400; PMID:9572993
      A:Accession: T09456
      A:Status: preliminary; translated from GB/EMBL/DBJ
      A:Molecule type: mRNA
      A:Residues: 1-3623 <KOZ>
      A/Cross-references: EMBL:AF034611; NID:93929528; PIDN:AAC82612.1; PID:93929529
      C/Genetics:
      A/Map position: 10p12
      C/Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
      C/Keywords: receptor; vitamin B12 uptake
      F:1-24/Domain: signal sequence #status predicted <SIG>
      F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
      F:436-467/Domain: EGF homology <EGF>

      Query Match
      Best Local Similarity 9.4%; Score 174.5; DB 2; Length 3623;
      Matches 53; Conservative 26; Mismatches 64; Indels 23; Gaps 8;

      QY
      15 GQRTGTRASNSK-----LQLSD--KEONGVDPFRHRYVTISGNSIH----- 59
      2173 GRCGSHASTLFTSDNQMFQFISDHSNEGQFKIKYBAKSLACGANVYIHADAGAYV 2232

      Db
      2173 GRCGSHASTLFTSDNQMFQFISDHSNEGQFKIKYBAKSLACGANVYIHADAGAYV 2232

      QY
      60 -SPKPPHTPRNNVLMRLVAVDENVRITLTPERGLDEPDIDCKYFVEVE--PSD 116
      2233 TSPNHPNPPHADCIWLAAPPE-TRIOLQFEDREDIVTBN--CTSNVLELRDGVSD 2289

      Db
      2233 TSPNHPNPPHADCIWLAAPPE-TRIOLQFEDREDIVTBN--CTSNVLELRDGVSD 2289

```



Qy 117 GSVLGRMGSGTVPKQTSKGNHIRIRFVSDYFSPSGFCHYSI 162  
 Db 2290 APLISKFCGT-SLPSSQMSSEGVMLRFRSDN-SPTHVGFRAKYSI 2333

## RESULT 11

108618  
 intrinsic factor-B12 receptor CUBILIN precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 02-Aug-2002

C/Accession: T08618

R/Mostrarup, S.K.; Kozuyaki, R.; Kristiansen, M.; Kayser, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998

A/Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies

A/Reference number: Z16459; MUID:98148073; PMID:9478979

A/Accession: T08618

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-3623 <MOE>

A/Cross-references: EMBL:AF022247; NID:g3834379; PIND:AACT1661.1; PID:g3834380

C/Genetics:

A/Gene: CUBILIN

C/Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

C/Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>

F.133-164/Domain: EGF homology <EGF1>

F.436-467/Domain: EGF homology <EGF>

Query Match 8.7%; Score 160; DB 2; Length 3623;  
 Best Local Similarity 26.8%; Pred. No. 0.00022;

Matches 90; Conservative 44; Mismatches 130; Indels 72; Gaps 23;

Qy 31 QLSDDKQNGVQDPREHVRVITISGSGISHSPKFPPTPRNNVLRVAVDENVRIOQLTF 90  
 Db 924 KFSSDKLECG-----EVLTRAS-TGIISSPGHNVYRGVNCVTHVY-VQRGQILRIEF 974  
 Qy 91 DERGLEDEPDICKYDFVEVEEBSGSGVLGRMGSGTVPKQTSKGNHIRIRFVSDYF 150  
 Db 975 SS-FVLEFHYV--CTNDYLEIETVDTAQTFLRYCGK-SIPSLTISNSNISKILFVSDSL 1030  
 Qy 151 PSEPGFCYH-----STIMPQVET-----TSPSVLP-----PS-----LSLDLNNAVT 191  
 Db 1031 AHE-GFSINVAIDASSVCLDYTDNFGMLSSPN-FPNVYFSNMECIYRIVGLNQQLAL 1088  
 Qy 192 AFS--TLBELIRYLEPDRMQVLDLSLYKPTQLGKALYKSKSVNMLLKEEVKLY- 248  
 Db 1089 HFTPTLEDYFGSGQVDVEI-ROGGR-TSPVIG---IY---CGSVLPRPTIISHNKML 1141  
 Qy 249 -----SCTPRNFSVSIIEELKRTDTITWPGCLLVKRCGNCACCLHNCNECQVPRKVT 302  
 Db 1142 KFESDAALTAQFSA-----YWDGS--STGCGGN-----LTTPGVLTSPNPM 1183  
 Qy 303 KKHYE---VLQRPRTGVKGLHKSITDVALHHEHC 335  
 Db 1184 PYHSSBCTYRLKLSHG-SPELEFQDPLHHEHSC 1218

## RESULT 12

A55362

procollagen I C-proteinase enhancer protein precursor - human

C/Species: Homo sapiens (man)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 05-Nov-1999

C/Accession: A55362

R/Takahara, K.; Kessler, E.; Biniaminov, L.; Bruesel, M.; Eddy, R.L.; Jani-Sait, S.; Shaw

J. Biol. Chem. 269, 26280-26285, 1994

A/Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, F

A/Reference number: A55362; MUID:95014462; PMID:7523404

A/Accession: A55362

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-449 <TAK>

A/Cross-references: GB:IJ3799; NID:g642907; PIND:AAA61949.1; PID:g642908

C/Genetics:

A/Gene: GDB:PCOLCE

A/Cross-references: GDB:305468; OMIM:600270

A/Map position: 7q21.3-7q22

C/Superfamily: C1r/C1s repeat homology

C/Keywords: extracellular protein; glycoprotein; pyroglutamic acid

F.1-25/Domain: signal sequence #status predicted <SIG>

F.26-449/Product: #status predicted <MAT>

F.37-146/Domain: C1r/C1s repeat homology <C1R1>

F.159-270/Domain: C1r/C1s repeat homology <C1R2>

F.26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

F.29,431/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.5%; Score 158; DB 2; Length 449;  
 Best Local Similarity 34.5%; Pred. No. 2.2e-05;

Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;

Qy 56 GSISPKFPPT-YPRNNVLRVAVDENVRIOQLTFDERFGLDEPDICKYDFVEV--- 111  
 Db 168 GTLTTPWPESDYPRGSGSHHITAPPDQV-IALTF-EKFDLE--PTTCRYDSVSFNG 223  
 Qy 112 EEPDGSVLGRMGSGTVPKQTSKGNHIRIRFVSDYFSPSGFCHYSIIM----- 164  
 Db 224 AVSDSRRLGKFGCD-AVPGSISEGNELVQVFSDLSTVAD-GFSASYKTLPRGTAKG 281  
 Qy 165 --PQVETTSFVS-LPPSS 180  
 Db 282 QGPGKRGTEBPVKLPPKS 300

## RESULT 13

A39288

dorsal-ventral patterning protein tollid (BC 3.4.24.-) - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C/Accession: A39288

R/Shmell, M.J.; Ferguson, B.L.; Childs, S.R.; O'Connor, M.B.

Cell 67, 469-481, 1991

A/Title: The Drosophila dorsal-ventral patterning gene tollid is related to human bone

A/Reference number: A39288; MUID:92034970; PMID:1840509

A/Accession: A39288

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1057 <SHI>

A/Cross-references: GB:M76976; NID:g157305; PIND:AAA28491.1; PID:g157306

C/Genetics:

A/Gene: FlyBase:tlid

A/Cross-references: FlyBase:FBgn0003719

C/Superfamily: dorsal-ventral patterning protein tollid; astacin homology; C1r/C1s rep

C/Keywords: duplication; hydrolase; metalloproteinase; zinc

F.133-329/Domain: astacin homology <AST>

F.352-464/Domain: C1r/C1s repeat homology <C1R1>

F.468-578/Domain: C1r/C1s repeat homology <C1R2>

F.585-620/Domain: EGF homology <EG1>

F.624-740/Domain: C1r/C1s repeat homology <C1R3>

F.747-782/Domain: EGF homology <EG2>

F.787-896/Domain: C1r/C1s repeat homology <C1R4>

F.900-1013/Domain: C1r/C1s repeat homology <C1R5>

F.221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted

F.222/Active site: Gln #status predicted

Query Match 8.3%; Score 153; DB 1; Length 1057;  
 Best Local Similarity 33.3%; Pred. No. 0.00018;

Matches 47; Conservative 28; Mismatches 54; Indels 12; Gaps 7;

Qy 13 LAGRTGFRASNSKQLQSSDKQNGVQDPREHVR-----VTISGSGISHSPKFPPTYP 68  
 Db 432 VSGSVITTTQSRMLNTVNRNAAAGYGRFK-AREVVGCGDKTKTKQSDISPYPMDM 490  
 Qy 69 RNMLVRLVAVDENVRIOQLTFDERFGLDEPDICKYDFVEVE--PSDGSVLGRMGCS 126  
 Db 491 PDKECVRIITAPD-NHQVALKF-QSFLE--KHGCAVDFEIRDGNHSDRLIGRFGCD 546

```

QY      127 GTVPGKQTSKGNHRIREFVSD 147
          | : : | : |||||
Db      547 KLPNIKT-RSNQMYIREVSD 566

```

RESULT 14

polypeptide - African clawed frog  
 C,Species: *Xenopus laevis* (African clawed frog)  
 C,Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 03-Feb-2003  
 C,Accession: T30337  
 R,Yang, J.C.; Lindsay, L.J.; Hedrick, J.L.  
 submitted to the EMBL Data Library, March 1998  
 A,Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from *Xenopus laevis* oocytes.  
 A,Reference number: Z20829  
 A,Accession: T30337  
 A,Status: preliminary; translated from GB/EMBL/DBJ  
 A,Molecule type: mRNA  
 A,Residues: 1-1524 <YAN>  
 A,Cross-references: EMBL:U81290; NID:S2981640; PID:S281641; PIDN:AA24717.1  
 C,Superfamily: trypsin related polypeptide; trypsin homology

Query Match	8.0%;	Score 147.5;	DB 2;	Length 1524;
Best Local Similarity	28.7%;	Pred. No. 0.00082;		
Matches 54;	Conservative 34;	Mismatches 73;	Indels 27;	Gaps 10;

```
QY      GSJHSPEFPHITYRRNNVLVWRLVAVDENRILUTDEEFGJEDPEDICKDFPVE-EEP 114
Db      439 GMJTSFPYPPRYLRTKCSW-IIEAPENHIVLKFEED-FNVEYGHG--CIYDAVEYIDGA 494
QY      115 SDGSVLGRWGSGSTVBCKQSKGNHRIRFVSDEYFPSEPGFCIHYSIMPO-----VT 168
Db      495 EEKQLARLCGY-TLPDPISSPENTMLIRFKTD-MENSYPGPKVFSPVEREKQFSLPVD 552
QY      169 ETTSPSVLPSPSSISLDLLNNA-VTAFSTIEELIRLEPD---RKQVDL-----DS 214
Db      553 DFTLTSLTHPRALAIADVCGMAPTPRMWLPRIVGGEASPNMSWPQVOIFPLRTFHCEGA 612
QY      215 LYKPTQOL 222
Db      613 IISPQMIL 620
```

## RESULT 15

Na-reactive factor (EC 3.4.21.-) 2 precursor - human  
 A:Accession: A59271  
 N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)  
 C:Species: Homo sapiens (man)  
 C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000  
 A:Accession: A59271  
 R:Thiel, S.; Vornpu-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Laursen, S.B.; Poulsen, K.  
 Nature 386, 506-510, 1997  
 A:Title: A second serine protease associated with mannan-binding lectin that activates C  
 A:Reference number: A59271; MUID:97242412; PMID:9087741  
 A:Accession: A59271  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-686 <JUN>  
 A:Cross-references: GB:U09926; NID:G4007626; PIDN:CA71059.1; PID:G4007627  
 A:Experimental source: tissue liver  
 A:Note: submitted to GenBank, December 1996  
 A:Note: parts of this sequence, including the amino end of the mature protein, were de  
 C:Genetics:  
 A:Gene: GDB:MASP2  
 A:Cross-references: GDB:6071500  
 A:Map position: 1p36.2-1p36.3  
 C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H  
 C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-444,445-686/Product: Ra-reactive factor 2 #status predicted <M>  
 F:15-114/Domain: C1r/C1s repeat homology <C1R1>  
 F:142-180/Domain: EGF homology <EGF>

F:184-293/Domain: C1r/C1s repeat homology <C1R2>  
F:300-361/Domain: complement factor H repeat homology <FH1>  
F:366-430/Domain: complement factor H repeat homology <FH2>  
F:445-679/Domain: trypsin homology <TRY>  
F:72-90,143-155,152-165,167-180,184-211,241-259,340-348,328-361,366-412,396-430,434-552  
F:158/Modified site: erythro-beta-hydroxyasparagine (Asp) #status predicted  
F:444-445/Cleavage site: Arg-Ile (autolytic) #status predicted  
F:463,532,633/Active site: His, Asp, Ser #status predicted

Query Match	7.9%	Score 145.5	DB 1	Length 686
Best Local Similarity	30.8%	Pred. No. 0.00043		
Matches 33	Conservative 27	Mismatches 42	Indels 5	Gaps 4

[illegible]

Search completed: May 27, 2004, 15:47:23  
Job time : 15 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 15:38:06 ; Search time 10.5 Seconds  
(without alignments)  
1710.877 Million cell updates/sec

Title: US-09-818-943-2  
Perfect score: 1848  
Sequence: 1 MLILGLLTSALAGRTG.....DVALLHHEGDCVCGRNAGG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	10.3	707	1	BMP1_XENLA
2	183.5	9.9	928	1	NPPI_XENLA
3	181	9.8	986	1	BMP1_HUMAN
4	181	9.8	991	1	BMP1_MOUSE
5	176	9.5	923	1	NPPI_HUMAN
6	174	9.4	1022	1	TID_BRAR
7	172	9.3	922	1	NPPI_RAT
8	169	9.0	923	1	NPPI_MOUSE
9	167	9.0	914	1	NPPI_CHICK
10	163.5	8.8	616	1	SPAN_STRPU
11	158	8.5	449	1	PCOI_HUMAN
12	155.5	8.4	925	1	NPPI_RAT
13	155.5	8.4	931	1	NPPI_MOUSE
14	155.5	8.4	931	1	NPPI_MOUSE
15	153.5	8.3	326	1	VEGD_RAT
16	153	8.3	1057	1	TID_DROME
17	147.5	8.0	704	1	CRAR_MOUSE
18	145.5	7.9	686	1	MAS2_HUMAN
19	145.5	7.9	3565	1	CSM1_HUMAN
20	144.5	7.8	597	1	BP10_PARLI
21	144	7.8	699	1	CRAR_HUMAN
22	137.5	7.4	705	1	CIR_HUMAN
23	136.5	7.4	468	1	PCOI_RAT
24	136	7.4	354	1	VEGD_HUMAN
25	135.5	7.3	358	1	VEGD_MOUSE
26	133.5	7.2	468	1	PCOI_MOUSE
27	132	7.1	415	1	VEGD_MOUSE
28	131.5	7.0	3564	1	CSM1_MOUSE
29	130	7.0	639	1	BMP1_MOUSE
30	128	6.9	277	1	TSG6_HUMAN
31	127	6.9	419	1	VEGD_HUMAN
32	125.5	6.8	245	1	PDGB_FELCA
33	124.5	6.7	3670	1	CSM3_HUMAN

34	123	6.7	275	1	TSG6_MOUSE
35	119.5	6.5	3487	1	CSM2_HUMAN
36	117.5	6.4	276	1	TSG6_RABIT
37	114.5	6.2	226	1	PDGA_XENLA
38	113	6.1	695	1	CASP_MESAU
39	112.5	6.1	241	1	PDGB_HUMAN
40	111.5	6.0	164	1	VEGA_CAVPO
41	111.5	6.0	226	1	TSG1_SMSAV
42	109	5.9	855	1	ST14_HUMAN
43	108.5	5.9	148	1	VEGH_ORPN7
44	108	5.8	2796	1	CSM3_MOUSE
45	105.5	5.7	207	1	VEGB_HUMAN

## ALIGNMENTS

RESULT 1	ID	BMPI_XENLA	STANDARD;	PRT;	707 AA.
AC	P98070;	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).				
OS	Xenopus laevis (African clawed frog).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;				
CC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Embryo; PubMed=8262384;				
RX	MEDLINE=94085787; PubMed=8262384;				
RA	Maeno M., Xue Y., Wood T.L., Ong R.C., Kung H.F.;				
RT	"Cloning and expression of cDNA encoding Xenopus laevis bone				
RT	morphogenetic protein-1 during early embryonic development.";				
RL	Gene 134:257-261 (1993).				
CC	-1- FUNCTION: Involved in pattern formation in gastrula and later				
CC	differentiation of developing organs.				
CC	-1- DEVELOPMENTAL STAGE: Blastula, early gastrula and hatched				
CC	tadpoles; little or no expression in morula and late gastrula.				
CC	-1- SIMILARITY: Belongs to peptidase family M12A.				
CC	-1- SIMILARITY: Contains 3 CUB domains.				
CC	-----				
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
DR	EMBL; L12249; AAA16313.1; -				
DR	PIR; JC2218; JC2218.				
DR	HSSP; P00736; IAPQ.				
DR	MEROPS; M12.005; -				
DR	InterPro; IPR000152; Asx hydroxyl_1.				
DR	InterPro; IPR000859; CUB.				
DR	InterPro; IPR001881; BGF_Ca.				
DR	InterPro; IPR006209; BGF_Like.				
DR	InterPro; IPR006025; Pept_M_Zn_BS.				
DR	InterPro; IPR006026; Peptidase_M.				
DR	InterPro; IPR001506; Peptidase_M12A.				
DR	Pfam; PF01400; Aclatin; 1.				
DR	Pfam; PF000431; CUB; 3.				
DR	Pfam; PF00008; EGF; 1.				
DR	PRINTS; PR00480; ASTACTIN.				
DR	SMART; SM00042; CUB; 3.				
DR	SMART; SM00179; EGF_CA; 1.				
DR	SMART; SM00235; ZnMG; 1.				
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.				



DB 146 ECSNFTSSNGVSKPKYKPYKPNALBCTYIIIFA----PKNOEIV--LEPESFLEADS 198

RESULT 3

BMP1\_HUMAN STANDARD; PRT; 986 AA.

AC P13497; Q13822; Q13872; Q14874; Q99421; Q99422; Q99423; Q9UL38;

DT 01-JAN-1990 (Rel. 13, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)

DS (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (MTLd).

GN BMP1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

XP SEQUENCE FROM N.A. (ISOFORM BMP1-3).

RC TISSUE=Skin;

RX MEDLINE=96209868; PubMed=8643539;

RA Li S.W., Sieron A.L., Ferrala A., Hojima Y., Arnold W.V., Prockop D.J.;

RT "The C-proteinase that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogenic protein-1.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).

[2]

RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).

RX MEDLINE=89072730; PubMed=3201241;

RA Mooney J.M., Rosen V., Celeste A.J., Mltsock L.M., Whitters M.J., Ritz R.W., Hewick R.M., Wang E.A.;

RT "Novel regulators of bone formation: molecular clones and activities.";

RL Science 242:1528-1534(1988).

[3]

RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).

RC TISSUE=Placenta;

RX MEDLINE=96160316; PubMed=9500680;

RA Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;

RT "Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein-1.";

RL J. Mol. Med. 76:141-146(1998).

[4]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).

RC TISSUE=Placenta;

RX MEDLINE=95096114; PubMed=7798260;

RA Takahara K., Lyons G.E., Greenspan D.S.;

RT "Bone morphogenetic protein-1 and a mammalian tolloid homologue (MTLd) are encoded by alternatively spliced transcripts which are differentially expressed in some tissues.";

RL J. Biol. Chem. 269:32572-32578(1994).

[5]

RP DISULFIDE BOND IN METALLOPROTEASE DOMAIN.

RX MEDLINE=2136528; PubMed=11283002;

RA Garrigue-Antar L., Barker C., Kadler K.E.;

RT "Identification of amino acid residues in bone morphogenetic protein-1 important for procollagen C-proteinase activity.";

RL J. Biol. Chem. 276:26237-26242(2001).

CC -1- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II and III. Induces cartilage and bone formation.

CC -1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at Ala-I-Asp in type I and II procollagens and at Arg-I-Asp in type III.

CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

CC -1- ENZYME REGULATION: Activity is increased by the procollagen C-endopeptidase enhancer protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Name=BMP1-3;

CC IsoId=P13497-1; Sequence=Displayed;

CC Name=BMP1-1;

CC IsoId=P13497-2; Sequence=VSP\_005461, VSP\_005462;

CC Name=BMP1-2;

CC IsoId=P13497-7; Sequence=Not described;

CC Name=BMP1-4;

CC IsoId=P13497-3; Sequence=VSP\_005463, VSP\_005464;

CC Name=BMP1-5;

CC IsoId=P13497-4; Sequence=VSP\_005465, VSP\_005466;

CC Name=BMP1-6;

CC IsoId=P13497-5; Sequence=VSP\_005467, VSP\_005468;

CC Name=BMP1-7;

CC IsoId=P13497-6; Sequence=VSP\_005469, VSP\_005470;

CC -1- TISSUE SPECIFICITY: Ubiquitous.

CC -1- SIMILARITY: Belongs to peptidase family M12A.

CC -1- SIMILARITY: Contains 2 EGF-like domains.

CC -1- SIMILARITY: Contains 5 CUB domains.

CC -----

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CC -----

CC EMBL; U50330; AAA93462.1; -

CC EMBL; M22488; AAA51833.1; -

CC EMBL; Y08723; CAA69973.1; -

CC EMBL; Y08724; CAA69974.1; -

CC EMBL; Y08725; CAA69975.1; -

CC EMBL; L35278; AAC41703.1; -

CC EMBL; L35279; AAC41710.1; -

CC PIR; A37278; B58788.

CC HSSP; P00736; IAPQ.

CC MEROPS; M12.005; -

CC Genew; HGNC:1067; BMP1.

CC MIM; 112264; -

CC GO; GO:0005576; C:extracellular; NAS.

CC GO; GO:0008237; F:metallopeptidase activity; NAS.

CC GO; GO:0001502; P:cartilage condensation; TAS.

CC GO; GO:0007275; P:development; TAS.

CC InterPro; IPR000152; Asx\_hydroxyl\_S.

CC InterPro; IPR001881; EGF\_Ca.

CC InterPro; IPR000859; CUB.

CC InterPro; IPR006209; EGF\_Like.

CC InterPro; IPR006025; EGF\_Like.

CC InterPro; IPR006026; Peptidase\_M.

CC InterPro; IPR001506; Peptidase\_M12A.

CC Pfam; PF00431; CUB; 5.

CC Pfam; PF00008; EGF; 2.

CC PRINTS; PR00460; ASTACTIN.

CC SMART; SM00042; CUB; 5.

CC SMART; SM00179; EGF\_CA; 2.

CC SMART; SM00235; ZnMc; 1.

CC PROSITE; PS00010; ASX\_HYDROXYL; 2.

CC PROSITE; PS01180; CUB; 5.

CC PROSITE; PS00022; EGF\_1; FALSE\_NEG.

CC PROSITE; PS01186; EGF\_2; 2.

CC PROSITE; PS50026; EGF\_3; 2.

CC PROSITE; PS01187; EGF\_CA; 2.

CC PROSITE; PS00142; ZINC\_PROTEASE; 1.

CC Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;

CC Hydrolyase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;

CC Glycoprotein; Zymogen; Alternative splicing.

CC SIGNAL

CC FT PROPEP 23 120 POTENTIAL.

CC FT CHAIN 121 986 BONE MORPHOGENETIC PROTEIN 1.

CC FT DOMAIN 121 321 METALLOPROTEASE.

CC FT DOMAIN 322 434 CUB 1.

CC FT DOMAIN 435 546 CUB 2.

CC FT DOMAIN 547 588 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

CC FT DOMAIN 591 703 CUB 3.

CC FT DOMAIN 704 743 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

CC FT DOMAIN 747 859 CUB 4.

```

FT DOMAIN 860 976 CUB 5.
FT METAL 213 213 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 214 214 BY SIMILARITY.
FT METAL 217 217 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 223 223 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 183 186 BY SIMILARITY.
FT DISULFID 322 348 BY SIMILARITY.
FT DISULFID 375 397 BY SIMILARITY.
FT DISULFID 435 461 BY SIMILARITY.
FT DISULFID 488 510 BY SIMILARITY.
FT DISULFID 551 563 BY SIMILARITY.
FT DISULFID 559 572 BY SIMILARITY.
FT DISULFID 574 587 BY SIMILARITY.
FT DISULFID 591 617 BY SIMILARITY.
FT DISULFID 644 666 BY SIMILARITY.
FT DISULFID 707 718 BY SIMILARITY.
FT DISULFID 714 727 BY SIMILARITY.
FT DISULFID 729 742 BY SIMILARITY.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 599 599 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 703 730 DKDCSKDNGCCQDDCVNTFGSYECQCR -> EKRALQPP
RGRPHQKFRVQKRNRPQ (in isoform BMP1-1).
FT VARSPLIC 731 986 /Ftid=VSP 005461.
Missing (in isoform BMP1-1).
FT VARSPLIC 245 302 /Ftid=VSP 005462.
Missing (in isoform BMP1-1).
FT VARSPLIC 303 986 /Ftid=VSP 005464.
Missing (in isoform BMP1-4).
FT VARSPLIC 589 622 /Ftid=VSP 005465.
Missing (in isoform BMP1-5).
FT VARSPLIC 623 986 /Ftid=VSP 005466.
Missing (in isoform BMP1-5).
FT VARSPLIC 703 717 /Ftid=VSP 005467.
Missing (in isoform BMP1-6).
FT VARSPLIC 718 986 /Ftid=VSP 005468.
Missing (in isoform BMP1-6).
FT VARSPLIC 703 823 /Ftid=VSP 005469.
Missing (in isoform BMP1-7).
FT VARSPLIC 824 986 /Ftid=VSP 005470.
Missing (in isoform BMP1-7).
FT CONFLICT 748 748 R -> N (IN REF. 4).
FT CONFLICT 934 934 D -> S (IN REF. 4).
SQ SEQUENCE 986 AA; 111248 MW; F89201913K3CBEA CRC64;

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Query Match 9.8%; Score 181; DB 1; Length 986;  
 Best Local Similarity 42.6%; Pred. No. 7.4e-07;  
 Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;

```

QY 55 NSGSHPPKPPHTPPRMVAVLVAVDENRVLQTDDEKGLDPPEDDICKVFEVER. 113
DB 599 NSGITSPGWEKPEYPPKNCIMQVLAPQ--YRISLQDP--FFTEGADVCKDFEVRSG 654
QY 114 -PSDGSVLGRWCGSGTVPGKOTSKGNHRIKRVFSDVEPSEPCICHY 160
DB 655 LTRDSLHKGKFGS-EKPEVITISQYNNMRYVEFSNDTV-SKSGFKAHF 700
DR

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```

RESULT 4
ID_BMP1_MOUSE STANDARD; PRT; 991 AA.
AC P98053;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bone morphogenetic protein 1 precursor (BC 3.4.24.19) (BMP-1)
DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
GN BMP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RX MEDLINE=94229342; PubMed=8174772;
RA Fukagawa M., Nobori S., Hogan B.L.M., Jones C.M.;
RT "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT which is related to the Drosophila dorsventral gene tolloid and
RT encodes a putative activin metalloendopeptidase.";
RL Dev. Biol. 163:175-183(1994).
CC -1- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
CC and III. Induces cartilage and bone formation.
CC -1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala-I-asp in type I and II procollagens and at Arg-I-asp in type
CC III.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- ENZYME REGULATION: Activity is increased by the procollagen C-
CC endopeptidase enhancer protein.
CC -1- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
CC and floor plate region of the neural tube. Less in developing
CC membranous and endochondral bone, submucosa of intestine, dermis
CC of skin and the mesenchyme of spleen and lung.
CC -1- SIMILARITY: Belongs to peptidase family M12a.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -1- SIMILARITY: Contains 5 CUB domains.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; L24755; AAA37306.1; -.
DR PIR; I49540; I49540.
DR HSSP; P00736; IAPQ.
DR MEROPS; M12.005; -.
DR MCD; MGT.88176; BMP1.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12a.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZMGC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.

```

KM Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;  
 KM Hydroxylase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;  
 KM Glycoprotein; Zymogen.  
 FT SIGNAL 1 25  
 FT PROPEP 26 125  
 FT CHAIN 126 991  
 FT DOMAIN 126 326  
 FT DOMAIN 327 439  
 FT DOMAIN 440 551  
 FT DOMAIN 552 593  
 FT DOMAIN 596 707  
 FT DOMAIN 708 748  
 FT DOMAIN 752 864  
 FT DOMAIN 865 981  
 FT METAL 218 218  
 FT ACT\_SITE 219 219  
 FT METAL 222 222  
 FT METAL 228 228  
 FT DISULFID 188 191  
 FT DISULFID 327 353  
 FT DISULFID 380 402  
 FT DISULFID 440 466  
 FT DISULFID 493 515  
 FT DISULFID 556 568  
 FT DISULFID 564 577  
 FT DISULFID 579 592  
 FT DISULFID 596 622  
 FT DISULFID 649 671  
 FT DISULFID 712 723  
 FT DISULFID 719 732  
 FT DISULFID 734 747  
 FT CARBOHYD 96 96  
 FT CARBOHYD 147 147  
 FT CARBOHYD 337 337  
 FT CARBOHYD 368 368  
 FT CARBOHYD 604 604  
 SQ SEQUENCE 991 AA; 111607 MW; 68A1847783A0B9E CRC64;  
 Query Match 9.8%; Score 181; DB 1; Length 991;  
 Best Local Similarity 42.6%; Pred. No. 7.5e-07;  
 Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;  
 QY 55 NGSIHSPKPTFPRNMYLVAVDENVRITLTFDRFGLEDEDDICKYDPEVEE- 113  
 DB 604 NGSTTSPEWPKETPRNKNCIMQLVAPTO-YRISLQFD--FPETEGNDVCKIDFEVAVSG 659  
 QY 114 -PDSGSYLGRWCGSGTVPGKQTSKGNHIRIRFVSDPEPSEPGFCIH 160  
 DB 660 LTADSKLHGKFCGS-EKPEVITSGNNMRVFKSDNTV-SKKGFRAHF 705  
 RESULT 5  
 NRPI\_HUMAN STANDARD; PRT; 923 AA.  
 AC 014786; 060461;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).  
 GN NRPI OR NRP OR VEGF165R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=97433084; PubMed=9288753;  
 RA He Z., Tessier-Lavigne M.,  
 RT "Neuropilin is a receptor for the axonal chemorepellent semaphorin  
 RL Cell 90:739-751(1997).  
 [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39.  
 RC TISSUE=Brain;  
 RX MEDLINE=96186099; PubMed=9529250;  
 RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;  
 RT "Neuropilin-1 is expressed by endothelial and tumor cells as an  
 RT isoform-specific receptor for vascular endothelial growth factor.";  
 RL Cell 92:735-745(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31.  
 RC TISSUE=Prostatic adenocarcinoma;  
 RX MEDLINE=20183929; PubMed=10688880;  
 RA Gagnon M.L., Bieleben D.R., Gechtman Z., Miao H.-Q., Takashima S.,  
 RA Soker S., Klagsbrun M.;  
 RT "Identification of a natural soluble neuropilin-1 that binds vascular  
 RT endothelial growth factor: In vivo expression and antitumor  
 RT activity.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).  
 RP [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=20309748; PubMed=10748121;  
 RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;  
 RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid  
 RT form of vascular endothelial growth factor (VEGF) and of placenta  
 RT growth factor-2, but only neuropilin-2 functions as a receptor for  
 RT the 145-amino acid form of VEGF.";  
 RL J. Biol. Chem. 275:18040-18045(2000).  
 CC -1- FUNCTION: The membrane-bound isoform 1 is a receptor involved in  
 CC the development of the cardiovascular system, in angiogenesis, in  
 CC the formation of certain neuronal circuits and in organogenesis  
 CC outside the nervous system. It mediates the chemorepellant  
 CC activity of semaphorins. It binds to semaphorin 3A. The PLGF-2  
 CC isoform of BGF. The VEGF-165 isoform of VEGF and VEGF-B  
 CC Coexpression with KDR results in increased VEGF-165 binding to KDR  
 CC as well as increased chemotaxis. It may regulate VEGF-induced  
 CC angiogenesis.  
 CC -1- FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to  
 CC inhibit its binding to cells. It may also induce apoptosis by  
 CC sequestering VEGF-165. May bind as well various members of the  
 CC semaphorin family. Its expression has an averse effect on blood  
 CC vessel number and integrity.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is  
 CC secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Membrane-bound;  
 CC IsoId=014786-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Soluble, SNRP1;  
 CC IsoId=014786-2; Sequence=VSP\_004339, VSP\_004340;  
 CC -1- TISSUE SPECIFICITY: The expression of isoforms 1 and 2 does not  
 CC seem to overlap. Isoform 1 is expressed by the blood vessels of  
 CC different tissues. In the developing embryo it is found  
 CC predominantly in the nervous system. In adult tissues, it is  
 CC highly expressed in heart and placenta; moderately in lung, liver,  
 CC skeletal muscle, kidney and pancreas; and low in adult brain.  
 CC Isoform 2 is found in liver hepatocytes, kidney distal and  
 CC proximal tubules.  
 CC -1- SIMILARITY: Belongs to the neuropilin family.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.  
 CC -1- SIMILARITY: Contains 1 MM domain.  
 CC -----  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC DR EMBL; AF018956; AAC51759.1; -;  
 CC DR EMBL; AF016050; AAC12921.1; -;  
 CC DR EMBL; AF145712; AAF44344.1; -;  
 CC PDB; 1KEX; 28-JAN-03.

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DR Genew; HGNC:8004; NRPL.
DR MIM; 602069; -.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.
DR GO; GO:0007411; P:axon guidance; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00421; FAS8_C.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_Type_C; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS8C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FAS8C_1; 2.
DR PROSITE; PS01286; FAS8C_2; 2.
DR PROSITE; PS00023; FAS8C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00060; MAM_2; 1.
DR PROSITE; PS00060; MAM_2; 1.
DR Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor; Alternative splicing; 3D-structure.
FT CHAIN 1 21 NEUROPILIN-1.
FT DOMAIN 22 923 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 857 879 POTENTIAL.
FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.
FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 842 842 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 642 644 EFP -> GIK (in isoform 2).
FT VARSPPLIC 645 923 /FTid=VSP_004339.
FT VARSPPLIC 645 923 Missing (in isoform 2).
FT CONFLICT 26 26 K -> E (IN REF. 1).
FT CONFLICT 749 749 D -> H (IN REF. 2).
FT CONFLICT 855 855 E -> D (IN REF. 2).
SQ SEQUENCE 923 AA; 103120 MM; ADEADCA849E5D57 CRC64;

Query Match 9.5%; Score 176; DB 1; Length 923;
Best Local Similarity 32.6%; Pred. No. 1.8e-06;
Matches 57; Conservative 24; Mismatches 68; Indels 26; Gaps 9;

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RESULT 6
TID_BRARE ID TID_BRARE STANDARD; PRT; 1022 AA.
AD 057460;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24.-)
DE (Mn1 fin protein).
GN TOLLID OR TLD OR MFN.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=gastrolula;
RX MEDLINE=98057457; PubMed=9395394;
RA Blader P., Rastegar S., Fischer N., Straehle U.;
RT "Cleavage of the BMP-4 antagonist chordin by zebrafish Tolloid.";
RL Science 278:1937-1940(1997).
RN [2]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=99307076; PubMed=10375503;
RA Connors S.A., Trout J., Ekker M., Mullins M.C.;
RT "The role of tolloid/min1 fin in dorsoventral pattern formation of the
zbrafish embryo.";
RL Development 126:3119-3130(1999).
RP -I- FUNCTION: Required for patterning ventral tissues of the tail. May
increase bone morphogenetic protein (BMP) activity at the end of
gastrulation by proteolytic cleavage of chordin and release of BMP
from inactive complexes.
CC -I- TISSUE SPECIFICITY: During gastrulation, accumulates around the
closing blastopore with greater expression ventrally. At the
animal pole, expressed in the ectoderm flanking the anterior
neural plate. At the 10-somite stage, expressed in the developing
tailbud and cranial neural crest. At the 20-somite stage, also
expressed in the hematopoietic system.
CC -I- SIMILARITY: Belongs to peptidase family M12A.
CC -I- SIMILARITY: Contains 2 EGF-like domains.
CC -I- SIMILARITY: Contains 5 CUB domains.
CC -I- SIMILARITY: Contains 5 CUB domains.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF027596; AAC60304.1; -.
CC HSSP; P35555; 1EMN.
CC MEROPS; M12.016; -.
DR ZFIN; ZDB-GENE-990415-265; tolloid.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZMGC_1.
DR PROSITE; PS00010; ASX_HYDROXYL_2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.

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	DR	PROSITE:	PS01186;	EGF_2; 2.	
	DR	PROSITE:	PSS0026;	EGF_3; 2.	
	DR	PROSITE:	PS01187;	EGF_CA; 2.	
	KV	Developmental protease,	ZINC_PROTEASE; 1.		
	KW	Metal-binding; Calcium;	Egf-like domain; Repeat; Signal; Glycoprotein;		
	KM	Znmoeg..			
	FT	SIGNAL	POTENTIAL.		
	FT	PROPEP	POTENTIAL.		
	FT	CHAIN	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN.		
	FT		METALLOPROTEASE (BY SIMILARITY).		
	FT	DOMAIN	CUB 1.		
	FT	DOMAIN	BEP-LIKE 1, CALCIUM-BINDING (POTENTIAL).		
	FT	DOMAIN	CUB 3.		
	FT		BEP-LIKE 2, CALCIUM-BINDING (POTENTIAL).		
	FT	DOMAIN	CUB 4.		
	FT	DOMAIN	CUB 5.		
	FT	METL	ZINC (CATALYTIC) (BY SIMILARITY).		
	FT	ACT SITE	BY SIMILARITY.		
	FT	METL	ZINC (CATALYTIC) (BY SIMILARITY).		
	FT	METL	ZINC (CATALYTIC) (BY SIMILARITY).		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	BY SIMILARITY.		
	FT	DISULFID	N-LINKED (GLCNAC. . . ) (POTENTIAL).		
	FT	CARBOND	N-LINKED (GLCNAC. . . ) (POTENTIAL).		
	FT	CARBOND	N-LINKED (GLCNAC. . . ) (POTENTIAL).		
	FT	CARBOND	N-LINKED (GLCNAC. . . ) (POTENTIAL).		
	SO	SEQUENCE	1022 AA; 115536 MW; A68CA1DDE41793B9 CRC64;		
	Query Match	Score 174;	DB 1;	Length 1022;	
	Best Local Similarity	41.7%;	Pred. No. 2.9e-06;		
	Matches 45;	Conservative 20;	Indels 8;	Gaps 6	
Oy	55	NCSTHSPKFPHTYPPNNMLVLAVDENVRQLTFDERFGLEDPDDICKDFVEVER-	113		
	: :   :   :	: :   :   :	: :     :		
Db	635	NGTITTPMPKPXYPPNKKCVMQVVAPQT_YRISMOF-EAFEBLEG--NEVCCKDYAEVRSG	690		
Oy	114	-PSDSVGSRMGCGGTVPKGOKSKGNHRIIRRVSEPFPSBPFCIHY	160		
	: : :   :   :	: : :   :   :	: : :   :   :		
Db	631	LSDSRLGKTCTG-T-EVPEVTISQYNMRIFKSNDTV-SKGGFAHF	736		
	RESULT 7				
	NRPI_RAT	STANDARD;	PRT;	922 AA.	
AC	Q9OMJ9;				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Neuropllin-1 precursor	(Vascular endothelial cell growth factor 165 receptor).			
GN	NRPL	Rattus norvegicus (Rat).			
OS	Rattus norvegicus	(Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Eukaryota; Metazoa;	Chordata).			

CC	Mammalia;Eutheria;	Rodentia;	Scturognathi;	Muridae;	Mutinae;	Rattus.
OX	NCT_TaxID=10116;	[1]				
RN	SEQUENCE FROM N.A.					
RP	STRAIN=Sprague-Dawley;					
RC	MEDLINE=97433085;	PubMed=9288754;				
RX	Kojodin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,	Ginty D.D.;	"Neuropilin III receptor";			
RA	Cell 90:753-762(1997).	-I FUNCTION:	Receptor involved in the development of certain neuronal circuits and in organogenesis outside the cardiovascular system.	In angiogenesis,	the formation of	certain neurons binds to semaphorin 3A, the pLGF-2 isoform of PGF, the VEGF-165 isoform of VEGF and VEGF-B. Coexpression with KDR results in increased VEGF-165 binding to KDR as well as increased chemotaxis. It may regulate VEGF-induced angiogenesis (By similarity).
CC	I SUBCELLULAR LOCATION:	Type I membrane protein.				
CC	-I TISSUE SPECIFICITY:	Found in the embryonic nervous system.				
CC	-I SIMILARITY:	Belongs to the neuropilin family.				
CC	-I SIMILARITY:	Contains 2 CUB domains.				
CC	-I SIMILARITY:	Contains 2 F5/F8 type C domains.				
CC	-I SIMILARITY:	Contains 1 MAM domain.				
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CC	EMBL; AF016296; AAC53337.1; -. HSSP; P12259; ICZT.					
DR	HSSP; P12259; ICZT.					
DR	InterPro; IPRO00859; CUB.					
DR	InterPro; IPRO00421; FA5B_C.					
DR	InterPro; IPRO08979; Gal_bind_likc.					
DR	InterPro; IPRO00998; MAM_domain.					
DR	Pfam; PF00431; CUB; 2.					
DR	Pfam; PF00754; PS_F8_type_C; 2.					
DR	Pfam; PF00629; MAM; 1.					
DR	PRINTS; PR00020; MAMDOMAIN.					
DR	SMART; SMO0042; CUB; 2.					
DR	SMART; SMO0231; FA5BC; 2.					
DR	SMART; SMO0137; MAM; 1.					
DR	PROSITE; PS01180; CUB; 2.					
DR	PROSITE; PS01285; FA5BC_1; 2.					
DR	PROSITE; PS01286; FA5BC_2; 2.					
DR	PROSITE; PS50022; FA5BC_3; 2.					
DR	PROSITE; PS00740; MAM_1; 1.					
DR	PROSITE; PSS0060; MAM_2; 1.					
KM	Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat; Receptor.					
KW	Signal.	1	21			POTENTIAL.
FT	CHAIN	22	922			NEUROFILIN-1.
FT	DOMAIN	22	855			EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	856	880			POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).					
FT	DOMAIN	881	922			CUB 1.
FT	DOMAIN	27	141			CUB 2.
FT	DOMAIN	147	265			F5/F8 TYPE C 1.
FT	DOMAIN	275	424			F5/F8 TYPE C 2.
FT	DOMAIN	431	583			MAM.
FT	DOMAIN	645	811			PROBABLY.
FT	DISULFD	27	54			PROBABLY.
FT	DISULFD	82	104			PROBABLY.
FT	DISULFD	147	173			PROBABLY.
FT	DISULFD	206	228			BY SIMILARITY.
FT	DISULFD	275	424			BY SIMILARITY.
FT	DISULFD	431	583			N-LINKED (GLCNAC...)
FT	CARBOND	150	150			(POTENTIAL).
FT	CARBOND	261	261			(POTENTIAL).
FT	CARBOND	300	300			N-LINKED (GLCNAC...)

FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 922 AA; 103082 MW; CCF6F82AD098B0F2E CRC64;

Query Match 9.3%; Score 172; DB 1; Length 922;  
 Best Local Similarity 31.5%; Pred. No. 3.7e-06;  
 Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;

QY 2 LLLGLLLTSLALAGORTGTRAESNLSSKQLQSDKEQNGVQDPHRRHVITSGNGSIHSP 61  
 DB 7 LLCATLALALALAG-----AFRSKCGG-----TIKENPGYLTSP 42

QY 62 KPEHTTFRNMVWLVRVAVDENVRIQLTDERGLEDDEDDICKYDFVEV--EPPSDGSV 119  
 DB 43 GYHSYHPSKCEWLIQAPPEYQRIINFPNFDLEDRD---CKDYVEVIDGENEGRL 99

QY 120 LGRWCGSGTVPGKOTSGNHRIRFVSDYFSPSGCIHYSIIM--PQVTER-TSPS 174  
 DB 100 WGFCKGK-IAPSPVSSGPFPLFIKPVSD-YETHGAGFSIRYELFKRGPECSQNYTAPT 155

RESULT 8  
 NRPI\_MOUSE STANDARD; PRT; 923 AA.  
 AC P97333;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropilin-1 precursor (A5 protein).  
 GN NRPI OR NRP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Embryonic brain;  
 RA MEDLINE=96353149; PubMed=8748368;  
 RX Kawakami A., Kitsuikawa T., Takagi S., Fujisawa H.;  
 RT "Developmentally regulated expression of a cell surface protein,  
 RT neuropilin, in the mouse nervous system.";  
 RL J. Neurobiol. 29:1-17(1996).  
 CC - FUNCTION: Receptor involved in the development of the  
 CC cardiovascular system, in angiogenesis, in the formation of  
 CC certain neuronal circuits and in organogenesis outside the nervous  
 CC system. It mediates the chemorepulsant activity of semaphorins. It  
 CC binds to semaphorin 3A, the PlGF-2 isoform of PGF, the VEGF-165  
 CC isoform of VEGF and VEGF-B. Coexpression with KDR results in  
 CC increased VEGF-165 binding to KDR as well as increased chemotaxis.  
 CC It may regulate VEGF-induced angiogenesis (By similarity).  
 CC - SUBCELLULAR LOCATION: Type I membrane protein.  
 CC - TISSUE SPECIFICITY: Nervous system.  
 CC - SIMILARITY: Belongs to the neuropilin family.  
 CC - SIMILARITY: Contains 2 CUB domains.  
 CC - SIMILARITY: Contains 1 F5/8 type C domains.  
 CC - SIMILARITY: Contains 1 MAM domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D50086; BAA08789.1; -.  
 CC HSSP: P12259; 1CZT.  
 CC MGD: MGI:106206; NRP.  
 CC GO: GO:0017154; F:semaphorin receptor activity; IGI.  
 CC InterPro: IPR000859; CUB.  
 CC InterPro: IPR000421; FAS5 C.  
 CC InterPro: IPR008979; Gal\_Bind\_Like.  
 CC InterPro: IPR000996; MAM\_domain.

DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00754; F5\_F8\_Type\_C; 2.  
 DR Pfam; PF00629; MAM; 1.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00231; FAS5C; 2.  
 DR SMART; SM00137; MAM; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01285; FAS5C\_1; 2.  
 DR PROSITE; PS01286; FAS5C\_2; 2.  
 DR PROSITE; PS50022; FAS5C\_3; 2.  
 DR PROSITE; PS00740; MAM\_1; 1.  
 DR PROSITE; PS50060; MAM\_2; 1.  
 KW Angiogenesis; Transmembrane; Glycoprotein; Neurexin; Signal; Repeat;  
 KM Receptor.

FT SIGNAL 1 21  
 FT CHAIN 22 923  
 FT DOMAIN 22 856  
 FT TRANSMEM 857 879  
 FT DOMAIN 880 923  
 FT DOMAIN 27 141  
 FT DOMAIN 147 265  
 FT DOMAIN 275 424  
 FT DOMAIN 431 583  
 FT DOMAIN 645 811  
 FT DISULFID 27 54  
 FT DISULFID 82 104  
 FT DISULFID 147 173  
 FT DISULFID 206 228  
 FT DISULFID 275 424  
 FT CARBOHYD 431 583  
 FT CARBOHYD 150 150  
 FT CARBOHYD 261 261  
 FT CARBOHYD 300 300  
 FT CARBOHYD 522 522  
 FT CARBOHYD 842 842  
 SQ SEQUENCE 923 AA; 103020 MW; 0644B8A170796808 CRC64;

Query Match 9.1%; Score 169; DB 1; Length 923;  
 Best Local Similarity 31.5%; Pred. No. 6.5e-06;  
 Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;

QY 2 LLLGLLLTSLALAGORTGTRAESNLSSKQLQSDKEQNGVQDPHRRHVITSGNGSIHSP 61  
 DB 7 LLCATLALALALAG-----AFRSKCGG-----TIKENPGYLTSP 42

QY 62 KPEHTTFRNMVWLVRVAVDENVRIQLTDERGLEDDEDDICKYDFVEV--EPPSDGSV 119  
 DB 43 GYHSYHPSKCEWLIQAPPEYQRIINFPNFDLEDRD---CKDYVEVIDGENEGRL 99

QY 120 LGRWCGSGTVPGKOTSGNHRIRFVSDYFSPSGCIHYSIIM--PQVTER-TSPS 174  
 DB 100 WGFCKGK-IAPSPVSSGPFPLFIKPVSD-YETHGAGFSIRYELFKRGPECSQNYTAPT 155

RESULT 9  
 NRPI\_CHICK STANDARD; PRT; 914 AA.  
 ID NRPI\_CHICK  
 AC P79755;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Neuropilin-1 precursor (A5 protein).  
 GN NRPI OR NRP.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=White Leghorn; TISSUE=Embryonic brain;  
 RX MEDLINE=95324761; PubMed=7601310;

RA Takagi S., Kaenya Y., Shimizu M., Matsura T., Tsuboi M., Kawakami A.,  
 RA Fujisawa H.;  
 RT "Expression of a cell adhesion molecule, neuropilin, in the  
 RT developing chick nervous system.";  
 RL Dev. Biol. 170:207-222(1995).  
 CC -1- FUNCTION: Receptor involved in the development of the  
 CC cardiovascular system, in angiogenesis, in the formation of  
 CC certain neuronal circuits and in organogenesis outside the nervous  
 CC system. It mediates the chemorepulsive activity of semaphorins (By  
 CC similarity). Seems to have calcium-independent cell adhesion  
 CC properties.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Developing nervous system; optic tectum  
 CC (layers D and E of SGFS), amacrine cells of retina, neurites of  
 CC dorsal root ganglia. Also expressed in nonneuronal cells, e.g.  
 CC blood vessels in the entire embryo.  
 CC -1- SIMILARITY: Belongs to the neuropilin family.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.  
 CC -----  
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 CC -----  
 CC EMBL: D45416; BAA08256.1; -;  
 CC DR HSSP: P12259; 1CZT.  
 CC DR InterPro: IPR000859; CUB.  
 CC DR InterPro: IPR000421; PA58 C.  
 CC DR InterPro: IPR008979; Gal\_Bind\_Like.  
 CC DR InterPro: IPR000998; MAM\_domain.  
 CC DR Pfam: PF00431; CUB; 2.  
 CC DR Pfam: PF00754; F5\_F8\_type\_C; 2.  
 CC DR Pfam: PF00629; MAM; 1.  
 CC DR PRINTS: PRO0020; MAMDOMAIN.  
 CC DR SMART: SM00042; CUB; 2.  
 CC DR SMART: SM00231; FA58C; 2.  
 CC DR SMART: SM00137; MAM; 1.  
 CC DR PROSITE: PS01180; CUB; 2.  
 CC DR PROSITE: PS01285; FA58C\_1; 2.  
 CC DR PROSITE: PS01286; FA58C\_2; 2.  
 CC DR PROSITE: PS50022; FA58C\_3; 2.  
 CC DR PROSITE: PS00740; MAM\_1; 1.  
 CC DR PROSITE: PS50060; MAM\_2; 1.  
 CC DR Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;  
 CC KM Receptor; Cell adhesion.  
 CC FT SIGNAL 1 18  
 CC FT CHAIN 19 914  
 CC FT DOMAIN 20 847  
 CC FT TRANSMEM 848 870  
 CC FT DOMAIN 871 914  
 CC FT DOMAIN 25 139  
 CC FT DOMAIN 145 263  
 CC FT DOMAIN 273 422  
 CC FT DOMAIN 429 581  
 CC FT DOMAIN 636 801  
 CC FT DISULFID 25 52  
 CC FT DISULFID 80 102  
 CC FT DISULFID 145 171  
 CC FT DISULFID 204 226  
 CC FT DISULFID 273 422  
 CC FT DISULFID 429 581  
 CC FT DISULFID 581 914  
 CC FT DISULFID 914 914  
 CC FT DISULFID 102480 MW; DD2BE6DFCBB68C CRC64;  
 CC SEQUENCE 914 AA; 102480 MW; DD2BE6DFCBB68C CRC64;  
 CC Query Match 9.0%; Score 167; DB 1; Length 914;  
 CC Best Local Similarity 28.8%; Pred. No. 9.4e-06;  
 CC Matches 51; Conservative 31; Mismatches 65; Indels 30; Gaps 9;  
 CC 50 VTISGNSHSPKPHPTYPNMLVWRLVAVDENVRQLTFDEKFGLEDEDDICKYDFV 109

DB 29 IKILSPYLTPGVPQSHYSQCEMLIQAPPEYQRLIMINPNPFDLEDD---CKYDV 85  
 QY 110 EV--EESPDSVIGRMCGSGTVPEKQTSKNHRIKRVSEYPPSEGFCHISITN--P 165  
 DB 86 EVIDGDNAEERLWNGKYCGK-IAPPPVLVSSGPYLFIRKVS-YETHGAGFSIRYEVFRGP 143  
 QY 166 QYVE--TTSVSLP-----PSSSLD-----LNNVTAFTLEELIRYLEPD 206  
 DB 144 ECKNFTSSGGMKSPGPPPKYFNSLECTYIIRAPKMSILLFESPE-----LEPD 195  
 RESULT 10  
 ID SPAN STREP STANDARD; PRT; 616 AA.  
 AC P98068;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-1998 (Rel. 36, Last annotation update)  
 DE SPAN protein precursor (EC 3.4.24.-).  
 GN SPAN.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxId=7668;  
 RX MEDLINE=92315921; PubMed=1618141;  
 RA Reynolds S.D., Angerer L.M., Pails J., Nasir A., Angerer R.C.;  
 RT "Early mRNAs, spatially restricted along the animal-vegetal axis of  
 RT sea urchin embryos, include one encoding a protein related to tollid  
 RT and BMP-1.";  
 RL Development 114:769-786(1992).  
 CC -1- TISSUE SPECIFICITY: Asymmetrically along the animal-vegetal axis  
 CC of the blastula.  
 CC -1- DEVELOPMENTAL STAGE: Very early blastula (between 16-cell stage  
 CC and hatching).  
 CC -1- SIMILARITY: Belongs to peptidase family M12A.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC -----  
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 CC -----  
 CC EMBL: M84144; AAA30072.1; -;  
 CC DR HSSP: P28825; 1IAF.  
 CC DR MEROPS: M12\_013; -;  
 CC DR InterPro: IPR000859; CUB.  
 CC DR InterPro: IPR006209; EGF\_Like.  
 CC DR InterPro: IPR006210; IEGF\_Like.  
 CC DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 CC DR InterPro: IPR006026; Peptidase\_M.  
 CC DR InterPro: IPR001506; Peptidase\_M12A.  
 CC DR Pfam: PF01400; Asclain; 1.  
 CC DR Pfam: PF00431; CUB; 2.  
 CC DR PRINTS: PRO0480; ASTACIN.  
 CC DR SMART: SM00042; CUB; 2.  
 CC DR SMART: SM00181; EGF; 1.  
 CC DR SMART: SM00235; ZNMG; 1.  
 CC DR PROSITE: PS01180; CUB; 2.  
 CC DR PROSITE: PS00022; EGF\_1; 1.  
 CC DR PROSITE: PS01186; EGF\_2; 1.  
 CC DR PROSITE: PS50026; EGF\_3; 1.  
 CC DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 CC KM Developmental protein; Repeat; Hydroxylase; Protease; Zinc; Embryo;  
 CC Metalloprotease; EGF-like domain; Signal.  
 CC FT SIGNAL 1 16  
 CC FT SIGNAL 16  
 CC POTENTIAL.

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FT PROPEP 17 93 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 94 616 SPAN PROTEIN.
FT DOMAIN 93 295 ARG/LYS-RICH (BASIC).
FT DOMAIN 94 295 METALLOPROTEASE.
FT DOMAIN 295 329 EGF-LIKE.
FT DOMAIN 340 450 CUB 1.
FT DOMAIN 451 502 THR-RICH.
FT DOMAIN 503 614 CUB 2.
FT METAL 190 190 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 191 191 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 194 194 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 200 200 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 299 315 BY SIMILARITY.
FT DISULFID 305 317 BY SIMILARITY.
FT DISULFID 319 328 BY SIMILARITY.
SQ SEQUENCE 616 AA; 67902 MW; 397CD923F9B98 CRC64;

Query Match 8.8%; Score 163.5; DB 1; Length 616;
Best Local Similarity 28.0%; Pred. No. 1.1e-05;
Matches 63; Conservative 30; Mismatches 85; Indels 47; Gaps 11;

QY 9 LTSALAGORTG-TRASNLSKXQLSDKX-----ONGVODRHRHV--TISGN- 55
DB 269 LNSRL-GQRTALSAADIELNRIYECDDVDCNNADECLNGYHDDCCVCPSSYSGLD 327
QY 56 -----GSIHSPKPHPTPRNNVLVWRLVAVDENRVLQTFDERF 94
DB 328 CQGGFTVRPADCSYRFTMTGETITSPNSNEDMTACVYELEG-PYGSTIELTF---L 383
QY 95 GLEDEPDIDCKYFVEVEEESDGVLCRWGCGSGTVEGKQTSKNHRIKRVSPDEPPS-- 152
DB 384 DMEIEETLCRYAVEVRKXDINSIGKFCGN-TLPPVQISSSNQMWVSFTSD---PSIT 439
QY 153 EPEFCIHYSTIMPOVT--ETTSPSVLPPSSLSDLLNNATVAST 195
DB 440 RRGFKATYVILLIQTTFVSTITLQTPPTSTITLQTNPSITTLQOT 484

RESULT 11
PCOL HUMAN STANDARD; PRT; 449 AA.
AC 015113; 014550;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
DE procollagen COOH-terminal proteinase enhancer) (Type I procollagen C-
DE proteinase enhancer protein).
GN PCOLCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95014462; PubMed=7523404;
RA Takahara K., Kessler E., Biniamov L., Brusel M., Eddy R.L.,
RA Jant-Sait S., Shows T.B., Greenspan D.S.,
RA "Type I procollagen COOH-terminal proteinase enhancer protein:
RT identification, primary structure, and chromosomal localization of the
RT cognate human gene (PCOLCE).";
RT J. Biol. Chem. 269:26280-26285 (1994).
RN 12
RP REVISIONS TO 56; 154 AND 373.
RA Kessler E.;
RL unpublished observations (FEB-2000).
RN 13
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Hirahara I., Syoutlida K., Harada K., Tomita M., Urakami K., Terai H.,
RA Morisaki N., Saito Y.,
RA "Smooth muscle cell derived procollagen C-protease enhancer protein.";
RT

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RL Cell Struct. Funct. 21:662-662 (1996).
RN 14
RP SEQUENCE FROM N.A.
RX MEDLINE=99018118; PubMed=9799793;
RA Gloeckner G., Scherer S., Schatevov R., Boright A.P., Weber J.,
RA Tsui L.-C., Rosenthal A.;
RT "Large-scale sequencing of two regions in human chromosome 7q22:
RT analysis of 650 kb of genomic sequence around the EPO and CUB1 loci
RT reveals 17 genes.";
RL Genome Res. 8:1060-1073 (1998).
RN 15
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99134301; PubMed=9933570;
RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
RT "Structural organization and expression patterns of the human and
RT mouse genes for the type I procollagen COOH-terminal proteinase
RT enhancer protein.";
RL Genomics 55:229-234 (1999).
RN 16
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ushed T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Miallhy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN 17
RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
RX MEDLINE=20092917; PubMed=10625689;
RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
RA Banda M.J.;
RT "Post-translational proteolytic processing of procollagen C-terminal
RT proteinase enhancer releases a metalloproteinase inhibitor.";
RL J. Biol. Chem. 275:1384-1390 (2000).
RN 18
RP FUNCTION: Binds to the COOH-terminal propeptide of type I
RN procollagen and enhances procollagen C-proteinase activity.
CC - FUNCTION: C-terminal processed part of PCPE (Ct-PCPE) may have an
CC metalloproteinase inhibitory activity.
CC - SUBCELLULAR LOCATION: Secreted.
CC - PTM: C-terminally processed at multiple positions.
CC - SIMILARITY: Contains 2 CUB domains.
CC - SIMILARITY: Contains 1 NTR domain.
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CC or send an email to license@sib-sib.ch).
DR EMBL; I33799; AAA61949.1; ALT SEQ.
DR EMBL; AB008549; BAA23281.1; -
DR EMBL; AF053356; AAC78800.1; -
DR EMBL; AF083655; AAD16041.1; -
DR EMBL; BC000574; AAH00574.1; -

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RESULT 13
NR2 HUMAN STANDARD; PRT; 931 AA.
ID NR2 HUMAN STANDARD; PRT; 931 AA.
AC 060462; 014820; 014821;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neutropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
GN NR2 OR VEGF165R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
RX MEDLINE=97470888; PubMed=9333348;
RT "Neutropilin-2, a novel member of the neutropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema III."
RT Neuron 19:547-559(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A22).
RC TISSUE=Brain;
RX MEDLINE=98188099; PubMed=9529250;
RT Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
RT "Neutropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";
RT Cell 92:735-745(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=20309748; PubMed=10748121;
RT Gluzman-Polcorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neutropilin-2 and neutropilin-1 are receptors for the 155-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neutropilin-2 functions as a receptor for the 145-amino acid form of VEGF."
RT J. Biol. Chem. 275:18040-18045(2000).
CC -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165 and VEGF-145 isoforms of VEGF, and the PlGF-2 isoform of RGF.
CC -1- SUBUNIT: Neutropilin-2 probably forms a heteromeric complex with neutropilin-1 in order to be a functional semaphorin 3C receptor.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=A22;
CC IsoId=O60462-1; Sequence=Displayed;
CC Name=A0;
CC IsoId=O60462-2; Sequence=VSP_004342;
CC Name=A17;
CC IsoId=O60462-3; Sequence=VSP_004341;
CC -1- SIMILARITY: Belongs to the neutropilin family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -----
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CC -----
DR EMBL; AF022859; AAC51788.1; -
DR EMBL; AF022860; AAC51789.1; -
DR EMBL; AF016098; AAC12922.1; -
DR HSSP; P12259; ICZT.
DR Genew; HGNC:8005; NR2P.
DR MIM; 602070; -
DR GO; GO:0005624; Cmembrane fraction; TAS.
DR GO; GO:0004872; F;receptor activity; TAS.

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DR GO; GO:0005021; F;vascular endothelial growth factor receptor. . .; TAS.
DR GO; GO:007411; P;axon guidance; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000421; FAS5 C.
DR InterPro; IPR008979; GalBindLike.
DR InterPro; IPR000938; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS5C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FAS5C_1; 2.
DR PROSITE; PS01286; FAS5C_2; 2.
DR PROSITE; PS50022; FAS5C_3; 2.
DR PROSITE; PS50060; MAM_2; 1.
DR PROSITE; PS50060; MAM_2; 1.
DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
KW Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 931
FT DOMAIN 21 864
FT TRANSMEM 865 889
FT DOMAIN 890 931
FT DOMAIN 28 142
FT DOMAIN 149 267
FT DOMAIN 277 427
FT DOMAIN 434 592
FT DOMAIN 642 802
FT DOMAIN 671 674
FT DISULFID 28 55
FT DISULFID 83 105
FT DISULFID 149 175
FT DISULFID 208 230
FT DISULFID 277 427
FT DISULFID 434 592
FT CARBOHYD 152 152
FT CARBOHYD 157 157
FT CARBOHYD 629 629
FT CARBOHYD 839 839
FT VARSPPLIC 809 813
FT VARSPPLIC 809 830
FT VARSPPLIC 809 830
FT CONFLICT 602 602
FT SEQUENCE 931 AA; 104830 MW; 270CBAE6A0A797C CRC64;
SQ
Query Match 8.4%; Score 155.5; DB 1; Length 931;
Best Local Similarity 32.1%; Pred. No. 8.4e-05;
Matches 42; Conservative 20; Mismatches 62; Indels 7; Gaps 4;
QY 34 SKEQNGVDPDRHEVVTISGSGSIHSPKFTPTPRNVLVAVDENVRIQLTPDR 93
DB 16 SHQVRGQDPDPCGGRGLNSKDGAYITSPGYPDYSHONCEVIYVAPEENQKIVNPNH 75
QY 94 FGLPEPEDICIKYDFVEVEPEPSDGS--VLGRKSGGTVPQKOTSGKNHRIKRVSDERYP 151
DB 76 FIEIKHD---CKYDIHIRDGSESADLGRKGN-IAPPTISSGSMLYIKFTSD-VAR 130
QY 152 SEFGFCIHYSI 162
DB 131 QAGGSLRVEI 141

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RESULT 14
NR2 MOUSE STANDARD; PRT; 931 AA.
ID NR2 MOUSE STANDARD; PRT; 931 AA.
AC 035375; 035373; 035374; 035376; 035377; 035378;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neutropilin-2 precursor (Vascular endothelial cell growth factor 165

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DE receptor 2).
EN NRP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).
RC STRAIN=BALB/C;
RX MEDLINE=93470888; PubMed=9331348;
RA "Chen H., Chetotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.,
RT "Neurophilin-2, a novel member of the neurophilin family, is a high
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema
RT III."
RL Neuron 19:547-559(1997).
CC -1- FUNCTION: High affinity receptor for semaphorins 3C, 3F, VEGF-165
CC and VEGF-145 isoforms of VEGF, and the PLGF-2 isoform of PGF.
CC -1- SUBUNIT: Neurophilin-2 probably forms a heteromeric complex with
CC neurophilin-1 in order to be a functional semaphorin E receptor.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named Isoforms=6;
CC Name=A22;
CC IsoId=035375-1; Sequence=Displayed;
CC Name=A0;
CC IsoId=035375-2; Sequence=VSP_004344;
CC Name=A5;
CC IsoId=035375-3; Sequence=VSP_004345;
CC Name=A17;
CC IsoId=035375-4; Sequence=VSP_004343;
CC Name=B0;
CC IsoId=035375-5; Sequence=VSP_004346;
CC Name=B5;
CC IsoId=035375-6; Sequence=VSP_004347;
CC -1- TISSUE SPECIFICITY: Expressed in developing CNS and in some
CC nonneural tissues including limb buds, developing bones, muscles,
CC intestinal epithelium, kidney, lung and submandibular gland.
CC -1- DEVELOPMENTAL STAGE: The expression pattern is very dynamic and is
CC developmentally regulated.
CC -1- SIMILARITY: Belongs to the neurophilin family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 FS/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -----
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CC -----
DR EMBL; AF022856; AAC53379.1; -
DR EMBL; AF022855; AAC53377.1; -
DR EMBL; AF022855; AAC53378.1; -
DR EMBL; AF022857; AAC53380.1; -
DR EMBL; AF022858; AAC53381.1; -
DR EMBL; AF022861; AAC53382.1; -
DR HSSP; P12359; 1CZT.
DR MGD; MGI:1100492; NRP2.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR008979; Gal Bind like.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; FS_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SMO0042; CUB; 2.
DR SMART; SMO0231; FA58C; 2.
DR SMART; SMO0137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C; 1; 2.

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[illegible]

